

A;Molecule type: DNA
A;Residues: 178-215 <RES>
A;Cross-references: UNIPARC:UPI00016A03C; GB: M37724; NID: 9183537; PID: AAA88047.1; PID: 16204
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 800-856 <RE2>
A;Cross-references: UNIPARC:UPI00016A03D; GB: M37725; NID: 9183538; PID: AAA88048.1; PID: 16204
A;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
structurally and functionally unrelated lipophilic antitumor drugs.
C;Genetics:
A;Gene: GDB:PGY1; MDR1
A;Map position: 7q11-7q21
A;Superfamily: multidrug resistance protein; ATP-binding cassette homology
C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; Phosphoprotein;
P;1-638-653-1280/Region: duplication; nucleotide binding motif B
P;1-59-350/Domain: hydrophobic <HLI>
P;351-637/Domain: hydrophobic <HLI>
P;110-604/Domain: ATP-binding cassette homology <ABC1>
P;127-434/Region: nucleotide-binding motif A (P-loop)
P;551-555/Region: nucleotide-binding motif B
P;38-708/Domain: linker <LN>
P;109-933/Domain: hydrophobic <HLI>
P;194-1280/Domain: hydrophobic <HLI>
P;1053-1249/Domain: ATP-binding cassette homology <ABC2>
P;1070-1077/Region: nucleotide-binding motif A (P-loop)
P;1196-1200/Region: nucleotide-binding motif B
P;91, 94, 99/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;163/Binding site: ATP (Lys) #status predicted
P;661, 667, 671, 681/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted
P;1076/Binding site: ATP (Lys) #status predicted

Query Match 96.4%; Score 6212.5; DB 1; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1238; Conservative 18; N mismatches 24; Indels 3; Gaps 1;

QY 1 MDLEEDRNGAEKRRNKFVFRANKSKDKRKERKPTVSPMFRTSYWILDAYAMVGTIAAI 60
DB 1 MDLEEDRNGAEKAKKCNPKFLANKSKDKRKERKPTVSPMFRTSYWILDAYAMVGTIAAI 60
QY 61 HGAGHPLMLVLFGDMTDTFANAGNGDLGALLFNTINSNITDTVPVMDLEEDMTRAYV 120
DB 61 HGAGHPLMLVLFGDMTDTFANAGNGDLGALLFNTINSNITDTVPVMDLEEDMTRAYV 120
QY 121 YSGTCAAGVLYAAVQSYFLCIAAGROTHIKRKOPFHAIHQEQIGMFDVHDGELENTRLD 180
DB 118 YSGTCAAGVLYAAVQSYFLCIAAGROTHIKRKOPFHAIHQEQIGMFDVHDGELENTRLD 177
QY 181 DVSKINEGCDKICMRPQMATEFGIGVFTGRKGLTIVTIALSPUGLSAAWAKTS 240
DB 178 DVSKINEGGCDKICMRPQMATEFGIGVFTGRKGLTIVTIALSPUGLSAAWAKTS 237
QY 241 SPTDEKLLAYAKAGAVAEVTLAATRVAGQKEELRNQLEAKRIGKIKAITANI 300
DB 238 SPTDEKLLAYAKAGAVAEVTLAATRVAGQKEELRNQLEAKRIGKIKAITANI 297
QY 301 SIGAFLLIYASYALAFWYCTTIVLKEYSTGQTVTFVFLIGAFPSVGASPTSEAFAN 360
DB 298 SIGAFLLIYASYALAFWYCTTIVLKEYSTGQTVTFVFLIGAFPSVGASPTSEAFAN 357
QY 361 ARGAFELIKKIDNPKPSIDSYSKSCHKPDNTKGENTLFPRVYHFSPSKRYTKILKGLNLKV 420
DB 358 ARGAYEIPFCLIDNPKPSIDSYSKSCHKPDNTKGENTLFPRVYHFSPSKRYTKILKGLNLKV 417
QY 421 QSGQTVALVNSGCCGCKSSTTQLMQLYDPREGMVSYDQGDQIRTINPREFLIGUVSQP 480
DB 418 QSGQTVALVNSGCCGCKSSTTQLMQLYDPREGMVSYDQGDQIRTINPREFLIGUVSQP 477
QY 481 VLFAATTIANTRYREDVMTDEIKAVKANAYDFTMKQPKDFLVRGERGAOLSGGQ 540
DB 478 VLFAATTIANTRYREDVMTDEIKAVKANAYDFTMKQPKDFLVRGERGAOLSGGQ 537

RESULT 2

DVXIC
multidrug resistance protein 1 - Chinese hamster

N;Alternate names: P-glycoprotein pep1

C;Species: Cricetomys griseus (Chinese hamster)

C;Date: 31-Dec-1990 #Sequence revision 30-Sep-1992 #text change 09-Jul-2004

C;Accession: A38696; C38696; E38696; S33758; T52823

R;Devinis, S.E.; Hassain, A.; Davide, J.P.; Malera, P.W.

J. Biol. Chem. 266: 4545-555, 1991

A;Title: Full length and alternatively spliced ppb-1 transcripts in multidrug-resistant

A;Accession: A38696

A;Molecule type: mRNA

A;Residues: 1-1276 <DEV>

A;Cross-references: C38696

A;Accession: A38696

A;Molecule type: mRNA

A;Residues: 108-1276

A;Cross-references: UNIPARC:UPI000008642; GB: M59254; PID: 9191156; PID: 9191154; PID:

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Gencore version 5.1.9

Om protein - protein search, using sw model.

Run on: November 14, 2006, 19:51:35 ; Search time 29.5576 Seconds

(without alignments)
4176.460 Million cell updates/sec

Title: US-10-619-359A-4

Perfect score: 6443

Sequence: 1 MDLGDGRNGAEEKQFFKLN.....LAQKGIVYFSMVSQAGAKRQ 1283

Scoring table: BL0SM62
Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Database : PIR 80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match Length	DB ID	Description
1	6212.5	96.4	1280	1 DVHJ1
2	5693	88.4	1276	1 DVHJ1
3	5677.5	88.1	1276	2 D34786
4	5303.5	82.3	1276	1 DVMS1
5	5203	81.2	1277	2 JH0502
6	5032	78.1	1104	1 DVMS1A
7	4953	76.9	1279	1 DVHJ3
8	4872.6	75.6	1276	1 DVMS2
9	486.6	75.5	1281	2 T48123
10	4838.5	75.1	1278	2 S41646
11	4430.5	68.8	1287	2 S55692
12	3238.5	50.3	1321	2 T42228
13	3234.5	50.2	1321	2 T42842
14	2892	44.9	1294	2 T19982
15	2846.5	44.2	1289	2 D87789
16	2832.5	44.0	1275	2 T31073
17	2756.5	42.8	1321	2 T22476
18	2754.5	42.8	1321	2 S22737
19	2714.5	42.1	655	1 DVH2C
20	2658	41.3	1283	2 A47377
21	2640	41.0	1286	2 T02187
22	2639.5	41.0	1292	2 T48007
23	2602.5	40.4	1278	2 E86155
24	2574.5	40.0	1302	2 A41249
25	2543.5	39.5	1229	2 DB5123
26	2540.5	39.4	1229	2 T52119
27	2531.5	39.3	1230	2 B88023
28	2511.5	39.0	1229	2 FB6155
29	2482.5	38.5	1302	2 B41249

Hypothetical prote multidrug resistant multidrug resistant P-glycoprotein PGP Hypothetical prote multidrug resistant Hypothetical prote E-glycoprotein C - Hypothetical prote E-glycoprotein 2 - multidrug resistant leptomycin B resis Hypothetical prote probable P-glycopr probable P-glycopr

DVHJ1 multidrug resistance protein 1 - human N;Alternate name: P-glycoprotein 1 Species: Homo sapiens (man) C;Date: 31-Dec-1990 #sequence revision 18-Aug-1995 T22094 C;Accession: A34914; PS0162; S15500; A2059; S43838; I52238; I65204 R;Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Roninson, I.B. J. Biol. Chem. 265, 506-514, 1990 A;Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin A;Reference number: A34914; PMID:9094448; PMID:1967175 A;Molecule type: DNA A;Residues: 1-1280 <CHE> A;Cross-references: UNIPARC:UPI000003BD16; GB:M29447; GB:J05168; NID:91 A;Accession: A34914 A;Reference number: PS0162 A;Molecule type: DNA A;Accession: PS0162 A;Molecule type: DNA A;Accessories: 1-22 <K12> A;Cross-references: UNIPARC:UPI0000174668 R;Kioka, N.; Yamano, Y.; Komaro, T.; Ueda, K. submitted to the EMBL Data Library, April 1991 A;Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression A;Accession: S15500 A;Accession: A34914 A;Molecule type: DNA A;Accessories: 1-22, R <K12> A;Cross-references: UNIPARC:UPI000016AD22; EMBL:X58723; PID:NID:934522; PID:CPA41558.1; PI R;Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I. Cell 47, 381-389, 1986 A;Title: Internal duplication and homology with bacterial transport proteins in the mdr A;Reference number: A25059; PMID:87028230; PMID:2876781 A;Accession: A25059 A;Molecule type: mRNA A;Accessories: 1-184, 'W', 186-1280 <CH2> A;Cross-references: UNIPARC:UPI0000039699; GB:M14758; NID:9187468; PID:R;Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F. Biochem. J. 299, 309-315, 1994 A;Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase A;Reference number: S43838; PMID:94220047; PMID:790941 A;Accession: S43838 A;Molecule type: protein A;Accessories: 65-689 A;Cross-references: UNIPARC:UPI00001746C9 R;Geckeler, V.; Weger, S.; Probst, H. Biochem. Biophys. Res. Commun. 169, 796-802, 1990 A;Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li. A;Reference number: I52238; PMID:9020529; PMID:1972623 A;Accession: I52238 A;Status: translated from GB/EMBL/DDJB

ALIGNMENTS

A; Molecule type: DNA	541 RIIARALYRNPKILLDEATSALDTSEAVQVALDKARKGRTTIVIAHRLSTVNADV 600
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A; Accession: 165204	Qy
A; Status: translated from GB/EMBL/DDJB	Db
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C; Comment: This is an integral membrane protein overproduced in multidrug-resistant cell	598 IAGFDGVIVEGNHDELMKEKGIFYFLVMTAGNEIELNAADESKSEIDLLENSND 657
structurally and functionally unrelated lipophilic antitumor drugs.	Qy
C; Genetics:	661 SGSSLIRKRSTRSRSVGSQGDPLKLTKEALDESIPVSFRIMKLNTEWPFYVGVFC 720
A; Cross-references: GDB:FGY1; MDR1	Db
A; Gene: GDB:FGY1; MDR1	658 SGSSLIRKRSTRSRSVGSQGDPLKLTKEALDESIPVSFRIMKLNTEWPFYVGVFC 717
A; Map references: GDB:120712; OMIM:171050	Db
A; Map position: multidrug resistance protein; ATP-binding cassette homology	721 ATINGLQPAFAVIFSKIGLIGFTRNDAETKRONSLFLSFLFLAIGLTSFPTFLQGFTF 780
C; Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;	Db
F1;1-638 F1;350-1280:Region: duplication	718 ATINGLQPAFAVIFSKIGLIGFTRNDAETKRONSLFLSFLFLAIGLTSFPTFLQGFTF 777
F4;9-350/Domain: hydrophobic <HB2>	Qy
F351-637/Domain: hydrophilic <HL1>	781 GRAGEILTKRLRYMVRFSMLQDVSFDDPNTGALTTRLANDAQVKGAGSGRRAIIT 840
F4;10-104/Domain: ATP-binding cassette homology <ABC1>	Db
F551-555/Region: nucleotide-binding motif A (P-loop)	778 GRAGEILTKRLRYMVRFSMLQDVSFDDPNTGALTTRLANDAQVKGAGSGRRAVIT 837
F4;27-434/Region: nucleotide-binding motif B	Qy
F7;09-993/Domain: hydrophobic <HB2>	841 QNIANLGTGIIISLIGWQWLTLLAVPIIAAGVEMKMSQALKDKELEGAGKIA 900
F6;338-708/Domain: linker <JIN>	Db
F7;99-1280/Domain: hydrophilic <HL2>	838 QNIANLGTGIIISLIGWQWLTLLAVPIIAAGVEMKMSQALKDKELEGAGKIA 897
F1;070-1077/Region: ATP-binding cassette homology <ABC2>	Qy
F1;1196-1200/Region: nucleotide-binding motif A (P-loop)	901 TEAIENFRTVYSLTOEOKFERNYDQSLQPVYRNSLRAKAIFGIFTFSFTOAMMYFSAGCF 960
F9;1-94/99/Binding site: carboxylate (Asn) (covalent) #status predicted	Db
F4;33/Binding site: ATP (lys) #status predicted	898 TEAIENFRTVYSLTOEOKFERNYDQSLQPVYRNSLRAKAIFGIFTFSFTOAMMYFSAGCF 957
F7;61-667, 673/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exp	Qy
F7;667, 673/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status	961 RFGAYLVAHKLMSEFDVLLVPSAVVYGMAGVQSSFAPDYAKVSAAHIMIIXTPL 1020
F1;076/Binding site: ATP (lys) #status predicted	Db
Query Match Score: 96.4%; Pred. No.: 0; Mismatches: 18; Conservative: 24; Indels: 3; Gaps: 1;	958 RFGAYLVAHKLMSEFDVLLVPSAVVYGMAGVQSSFAPDYAKVSAAHIMIIXTPL 1017
Best Local Similarity: 96.5%; Matches: 1238; Conservative: 18; Mismatches: 24; Indels: 3; Gaps: 1;	Qy
1 MDLEGDRGGAEKCKNEFKUNNKKSKDKKCKRKPTVSYESMERYSNWLDCIYMMYGTLLAI 60	1021 IDSYSTEMGLKNTLEGRNTFNVBNVFNTPTRDIPVQGLSLSEVKCOTLALVGSSCGKS 1080
1 MDLEGDRGGAEKCKNEFKUNNKKSKDKKCKRKPTVSYESMERYSNWLDCIYMMYGTLLAI 60	Db
Db	1018 IDSYSTEMGLMNTLEGRNTFGEVNTYPTREDIPVQGLSLSEVKCOTLALVGSSCGKS 1077
Qy	1081 TVVQLLERFYDPLAGKVLLDGKEIKOLNQVOMLRAHIGIVSOBPLIPDCSISENIAYGDNS 1140
Db	1078 TVVQLLERFYDPLAGKVLLDGKEIKOLNQVOMLRAHIGIVSOBPLIPDCSISENIAYGDNS 1137
Qy	1141 RVVSOQEIVRRAKEANHAFLSPLNKYSSTRVGDKTOLSGGOKORIAALARALVOPHIL 1200
Db	1138 RVVSOQEIVRRAKEANHAFLSPLNKYSSTRVGDKTOLSGGOKORIAALARALVOPHIL 1197
Qy	1201 LLDEATSDLTSEKVQVALDKAREGRCTIVIAHRLSTIONADLUVFONGRVKEHGTH 1260
Db	1198 LLDEATSDLTSEKVQVALDKAREGRCTIVIAHRLSTIONADLUVFONGRVKEHGTH 1257
Qy	1261 QOLLACKGTYXPSMYSVOGAKRQ 1283
Db	1258 QOLLACKGTYXPSMYSVOGAKRQ 1280
RESULT 2	
DVHYIC	
multidrug resistance protein 1 - Chinese hamster	
N; Alternative names: E-glycoprotein Pgp1	
C; Species: Crictetulus griseus (Chinese hamster)	
C; Date: 31-Dec-1990 #sequence revision 30-0-Sep-1992 #text change 09-Jul-2004	
C; Accession: A38696; C38696; Bi8696; A7126; S33768; I52823	
R; Devine, S.E.; Hussain, A.; Davide, J.P.; Melera, P.W.	
J; Biol. Chem. 266:4545-4555, 1991.	
A; Title: Full length and alternatively spliced ppb-1 transcripts in multidrug-resistant	
A; Reference number: A38696; PMID:91154265; PMID:1671863	
A; Accession: A38696	
A; Molecule type: mRNA	
A; Residues: 1-1276 <DEV>	
A; Cross-references: C38696	
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A; Residue: 108-1276 	
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Qy	478 VLFATTIENRYGRENTMDETEKAVKANAYDFIMKLPHKFDLIVGERGQLSGQKQ 537

301	SIGAAFLIIYASYALAFWYGTTLVLSKEYSIGIVLTVFFSVLIGAFPSVGOAPSIEBAFAN	3 60
295	SMCAAFLLIYASYALAFWYGTTSVLSKEYSIGIVLTVFFAVLIAPSIGAPSIEBAFAN	3 54
361	ARGAAFEIYFKIDNPKPSIDSYSKSGHKEPDNIKENLEFRNTYHESYSPSKREKTYKJLGSLNKV	4 20
Db	355 ARGAAFEIYFKIDNPKPSIDSFSKNGYKPNIKENLEFKNTHFSYSPSKREKTYKJLGSLNKV	4 14
421	QSGQTVALVGNSCGCKSSTVQLMQLDPTEGMNSVGDGDIRTNRVRFREIIGVVSQEP	4 80
Db	415 QSGQTVALVGNSCGCKSSTVQLMQLDPTEGMNSVGDGDIRTNRVRLRIGVVSQEP	4 74
481	VLFATTIAENIYGREDTYMDLEKAKEANAYDFIMKLPOKFDTLVGERGAOLSGGOKO	5 40
Db	475 VLFATTIAENIYGRENTYMDLEKAKEANAYDFIMKLPHKFDTLVGERGAOLSGGOKO	5 34
541	RIAIAARALVRNPKILLDEATSALDTESEAVVYQALDKARKGRTTIVIAHLSTVNRADV	6 00
Db	535 RIAIAARALVRNPKILLDEATSALDTESEAVVYQALDKARKGRTTIVIAHLSTVNRADV	5 94
601	IAGFDGGIVTEKGHNHDILMKEKGUYFKLVTMQTAGNEIELENADESKSEBDTLEMSHHD	6 60
Db	595 IAGFDGGIVTEKGHNHELMERKGUYFKLVTMQTAGNEIELENAGESENBEIDNLDMSSKD	6 54
661	SGSSLRKRSRSPSRVRSOGDRKLSTKEALDESIPVPSFWRIMKLNUITEWPYFVGVFC	7 20
Db	655 SASSLRRKRSRSPSRVRSOGDRKLSTKEALDESIPVPSFWRILKLNSSEWPFVGVFC	7 14
721	AINGGQPAFAVIFSKLIGITFRNDDAETKTRONSNLFSSLFLVGLIVSFITFFLQGFPE	7 80
Db	715 AINGGQPAFAVIFSKLIGITFRNDDAETKTRHDSNFSSLFLVGLIVSFITFFLQGFPE	7 74
781	GKAGEITTKRLRYMVFPSMLRDODVSFDDPKNTTGALTTRLANDAAQVKGAIGSRALAIT	8 40
Db	775 GKAGEITTKRLRYMVFPSMLRDODVSFDDPKNTTGALTTRLANDAAQVKGAIGSRALAVIT	8 34
841	QNIANLGTGIIISLYIGWQLTILLIAVPIIIAGVTEMOMISQALDKKELEGAKIA	9 00
Db	835 QNIANLGTGIIISLYIGWQLTILLIAVPIIIAGVTEMOMISQALDKKELEGAKIA	8 94
901	TEAIEFRFTVSLTOQKPEMYDQSLOQVYRZNSLRAKIIHGITFSITFOAMMYSYAGCF	9 60
Db	895 TEAIEFRFTVSLTOQKPEMYDQSLOQVYRZNSLRAKIIHGITFSITFOAMMYSYAGCF	9 54
961	RFGAYLVAHSLMSFEDVLLYPSAVVFGAMAVQVQSSPAPDYAKAVSAAHIMIETKTPL	10 20
Db	955 RFGAYLVAHSLMSFEDVLLYPSAVVFGAMAVQVQSSPAPDYAKAVSAAHIMIETKTPL	10 14
1081	TVVQOLLERFTDPLAKVLLDGKEIKIOLNVWLRHICGIVSOEPILFDGSISENTAYGDNS	11 40
Db	1075 TVVQOLLERFTDPLAKVLLDGKEIKIOLNVWLRHICGIVSOEPILFDGSISENTAYGDNS	10 80
1021	IDSYSTEGLKPNTLLEGNVTFEVVFTYPTRADIPVLQGLSLEVKGOTLALVSSGGGKS	11 34
Db	1015 IDSYSTEGLKPNTLLEGNVTFEVVFTYPTRADIPVLQGLSLEVKGOTLALVSSGGGKS	10 74
1141	RVVSOEETVRAKEANIAHAFESLPIKRYSTPGDKGTQLSGGOKORATARALVRPHIL	12 00
Db	1135 RVVSOEETVRAKEANIAHAFESLPIKRYSTPGDKGTQLSGGOKORATARALVRPHIL	11 94
1261	QLLAQKGIYFSMVSYQAGAKR	12 82
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C;date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004

C;accession: A34766; A35671
R;Devault, A.; Gros, P.

Mol. Cell. Biol. 10, 1652-1663, 1990

A;Title: Two members of the mouse mdr gene family confer multidrug resistance with over-

A;Reference number: A34786; PMID:90205845;
A;Accession: A34786
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-1276 <DEVS>

A;Cross-references: UNIPARC:UPI0000028C58; GB:M30697; NID:9199111; PIDN:

R;Hsu, S.-I. H.; Cohen, D.; Kirschner, L. S.; Lothestein, M.; Horwitz, S.B.

Mol. Cell. Biol. 10, 1596-1606, 1990

A;Title: Structural analysis of the mouse mdr1a (P-glycoprotein) promoter reveals the ba-

A;Reference number: A35671; MUID:90287150; PMID:1972547

A;Accession: A35671
A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 525, 'HV', 528-938, 'S', 940-1035, 'V', 1037-1276 <HSU>

A;Cross-references: UNIPARC:UPI0000046660; GB:M33581; NID:9199104; PIDN:AAA39514.1; PIDN:

C;Superfamily: multidrug resistance protein; ATP-binding cassette homology

C;Key words: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-loop

F;406-600/Domain: ATP-binding cassette homology <ABC1>

F;423-431/Region: nucleotide-binding motif A (P-loop)

F;57-551/Region: nucleotide-binding motif B

F;1049-1245/Domain: ATP-binding cassette homology <ABC2>

F;1066-1074/Region: nucleotide-binding motif A (P-loop)

F;1192-1196/Region: nucleotide-binding motif B

F;429/Binding site: ATP (Lys) #status predicted

F;1072/Binding site: ATP (Lys) #status predicted

Query Match, Score 5677.5; DB 2; Length 1276;

Best Local Similarity 87.1%; Pred. No. 1.e-311; Mismatches 78; Gaps 2;

Matches 116; Conservative 81; Indels 7; Gaps 2;

Qy 1 MDELEGDRGKAEKKNNKSKDKKERKPTVSPSMERYNSWLDKLMMYVTGLAAII 60

Db 1 NELUEDIGRAD-KNFSRKGKCSKEKEKCPAVSVLTMFRAGWLDRMLVGTGLAAI 59

Qy 61 RGGCLPLMLNVPDMTDPAAGNLGLDALLPRNTINSNITDTPVNLNEEDMTIRAY 120

Db 60 HGVALPLMLLIFSDMTDSFASVENVSK-----NSTNMSEADKRAMPFAKLEEMTTIAY 113

Qy 121 YSGIGAGVLYVAIVIQSPWCLAGROTHTKRCOFFHAIRMRQBGFDYHDYGESELNRLTD 180

Db 114 YTGIGAGVLYVAIVIQSPWCLAGROTHTKRCOFFHAIRMRQBGFDYHDYGESELNRLTD 173

Qy 181 DVSKINRGICGDKGIMFFPOMATPTGFTGFVGETRGWKLTLVILAIISPVLGSLSAWAKILS 240

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Qy 241 SFTDKELLAAYKAGVAAVEFLVALAIRTIAFGKKELERVNANLEERIGKIKATANI 300

Db 234 SFTDKELLAAYKAGVAAVEFLVALAIRTIAFGKKELERVNANLEERIGKIKATANI 293

Qy 301 SIGAAFLIAYASVALAFWYGTLLVLSKEYSIGIVLTVFSTVLGAFSVQASPSTIEAFAN 360

Db 294 SMCAGFLIAYASVALAWTGTLLVLSKEYSIGIVLTVFSTVLGAFSVQASPNTIEAFAN 353

Qy 361 ARGAAGFLPKLIDNKPDSISYSKSCHKPDNIKGNLEFRNVHPSYSRSKEVKILKGNLKV 420

Db 354 ARGAATEVKLIDNKPDSISYSKSCHKPDNIQGNLEFRNVHPSYSRSKEVKILKGNLKV 413

Qy 421 QSGQTVALVGNGSGCKGSTTQVMQLR1DPTEGNVSVDQDIFTINFLRIGVQSQEP 480

Db 414 KSGQTVALVGNGSGCKGSTTQVMQLR1DPTEGNVSVDQDIFTINFLRIGVQSQEP 473

Qy 481 VLFAATTAAENTRYGRDVTMDLEKAYKEANAYDFINKLPQKFDTLVGERAQLSGQKQ 540

Db 474 VLFAATTAAENTRYGRDVTMDLEKAYKEANAYDFINKLPQKFDTLVGERAQLSGQKQ 533

Qy 541 RIAJARALVRNPKILLDEATSALDTESEAVVOAALDKAREGRRTIVIAHRLSTVNADV 600

RESULTS 4

DVMS1

multidrug resistance protein 1 - mouse

N;Alternative names: P-glycoprotein 1

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 09-Jul-2004

R;Raymond, M.; Gross, P.

Proc Natl Acad Sci U.S.A. 86, 6488-6492, 1989

A;Title: Mammalian multidrug resistance gene: correlation of exon organization with str

A;Reference number: A33719; MUID:89367274; PMID:2570420

A;Accession: A33719
A;Molecule type: DNA

A;Residue: 1-1276 <RAY>

A;Cross-references: UNIPROT:PO6795; UNIPARC:UPI00000210D8

Cell 47, 371-380, 1986

A;Accession number: A25057

A;Molecule type: mRNA

A;Residue: 1-1276 <GRO>

Db	61	HGAGIPLMMLVFGDMTDTPANAGNLGDLGALLPNTNSNNITPTPVNLEEDTRYAYY	120	Qy	1198	LIDERASALDPESEKTVQLDKEAREGRTCVIARLSTQNADLIVFONGRVCEHGTII	1257
Qy	1118	YSIGIGAGIVVAAVTOVSFWCLAAAGRQHKLKRKOPFHAKMRQEIGMFDVHDGELENTR.LTD	177	Db	1201	LIDERASALDPESEKTVQLDKEAREGRTCVIARLSTQNADLIVFONGRVCEHGTII	1260
Db	121	YSIGIGAGIVVAAVTOVSFWCLAAAGRQHKLKRKOPFHAKMRQEIGMFDVHDGELENTR.LTD	180	Qy	1258	QQLLAQKGIVTSMVSYQAGKQ	1280
Qy	1778	DVSKCNEGGDKIGMPPQSKATPPTGFIVGFTREPKLTVLISPVLGSLSAWAKLIS	237	Db	1261	QQLLAQKGIVTSMVSYQAGKQ	1283
Db	181	DVSKCNEGGDKIGMPPQSKATPPTGFIVGFTREPKLTVLISPVLGSLSAWAKLIS	240				
Qy	238	SPTDKELLAYAKAGVAAETVLAARTVIAFGQKKEELVNKOLEEARIGIKKAIATANI	297				
Db	241	SPTDKELLAYAKAGVAAETVLAARTVIAFGQKKEELVNKOLEEARIGIKKAIATANI	300				
Qy	298	SIGAFLIYAYSTALAFWGTTLVLSKEISIGQVLTVPSVLGAFSTQASSPIEAPAN	357				
Db	301	SIGAFLIYAYSTALAFWGTTLVLSKEISIGQVLTVPSVLGAFSTQASSPIEAPAN	360				
Qy	358	ARGAAFEIPIKIDNKPKSDPSYSKSCHSKPKONIKENLEFRVNHFSYPSRSKEVKILGLNLKV	417				
Db	361	ARGAAFEIPIKIDNKPKSDPSYSKSCHSKPKONIKENLEFRVHFSPSREVKILGLNLKV	420				
Qy	418	QSGCTVALGVNGSGCGKSTTVQLMORLYDPTEGMVSYDGDODIRTNVRFLEITGVVSDP	477				
Db	421	QSGCTVALGVNGSGCGKSTTVQLMORLYDPTEGMVSYDGDODIRTNVRFLEITGVVSDP	480				
Qy	478	VLFATTIANNIYRGDVTNDEIEKAVERANADPIMKLPOKEFPLVGERGAQLSGGKQ	537				
Db	481	VLFATTIANNIYRGDVTNDEIEKAVERANADPIMKLPOKEFPLVGERGAQLSGGKQ	540				
Qy	538	RIAATARALYRNPCKLILLDEATSALDTESEAVYQVALDARKGRTTIVAHRLSTVRNADV	597				
Db	541	RIAALARALRNPKILLDEATSALDTESEAVYQVALDARKGRTTIVAHRLSTVRNADV	600				
Qy	598	IAGFDDGTVKEGNEDELMKKEGKTYFKLVTMOTAGNEIELENNADESEIDITLEMSHD	657				
Db	601	IAGFDDGTVKEGNEDELMKKEGKTYFKLVTMOTAGNEIELENNADESEIDITLEMSHD	660				
Qy	658	SGSSSLRKESTRSYRGSGQDQRKLSTKEALDESEPPSFWRMKNLNTTWPFLFVGFC	717				
Db	661	SGSSSLRKESTRSYRGSGQDQRKLSTKEALDESEPPSFWRMKNLNTTWPFLFVGFC	720				
Qy	718	AINGGLQPAFVPSKILGIPTANDDAETKRONSNLSSLFLVGLTYSITPFLGOTIF	777				
Db	721	AINGGLQPAFVPSKILGIPTANDDAETKRONSNLSSLFLVGLTYSITPFLGOTIF	780				
Qy	778	GKAGBILTKRLRYTFRSMRLODWSFWDDEKNTGALITRNLDAQVGAIGSLRAIT	837				
Db	781	GKAGBILTKRLRYTFRSMRLODWSFWDDEKNTGALITRNLDAQVGAIGSLRAIT	840				
Qy	838	QNIANLTGTIIISIYLGWQTLILIAVPIATAGVEMTNLSCQALKKELEGAGCIA	897				
Db	841	QNIANLTGTIIISIYLGWQTLILIAVPIATAGVEMTNLSCQALKKELEGAGCIA	900				
Qy	898	TEATENPRTVSLTOBKPERMYDOSLYPYRNRSLRKAHIGITTSFTQAMMFSYACCP	957				
Db	901	TEATENPRTVSLQTCQKPFHMDSLQVYPRNSLRKAHIGITTSFTQAMMFSYACCP	960				
Qy	958	RPGAYLVASLMSFDVLLVPSAVFGAMAVGQSSFADYAKVSAHHTMKTPL	1017				
Db	961	RPGAYLVASLMSFDVLLVPSAVFGAMAVGQSSFADYAKVSAHHTMKTPL	1020				
Qy	1018	IDSYSTEGLKPKNTLEGNTVNEVFNYPTRLDIPQGSLSVLVEKGOTALVSSGCRRS	1077				
Db	1021	IDSYSTEGLKPKNTLEGNTVNEVFNYPTRLDIPQGSLSVLVEKGOTALVSSGCRRS	1080				
Qy	1078	TIVVQOLLERFTDPLAKVLLDGKEIKQNLNTYOWLRAHLGIVVSQEPILFDCDSIRENTAYGNS	1137				
Db	1081	TIVVQOLLERFTDPLAKVLLDGKEIKQNLNTYOWLRAHLGIVVSQEPILFDCDSIRENTAYGNS	1140				
Qy	1118	RVVSEEEVRAKEANIHAPIESLPNKISTRVGDKGTLQSGGOKRIARALYRQPHL	1197				
Db	1123	RVVSEEEVRAKEANIHAPIESLPNKISTRVGDKGTLQSGGOKRIARALYRQPHL	1200				

RESULT 6
AAW44073
ID AAW44073 standard, protein; 1280 AA.

AC AAW44073;

XX 25-MAR-2003 (revised)

DT 26-JUN-1998 (first entry)

DB Human multidrug resistance P-glycoprotein MDR1.
KW Human; multidrug resistance P-glycoprotein; MDR1; prokaryotic homologue.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..640 /note= "MDR1-N from Fig 1"

FT 641..1280 /note= "MDR1-C from Fig 1"

FT PR 24-APR-1996; WO9740160-A1.

XX PN 20-OCT-1997.

XX PR 24-APR-1997; 97WO-NL000216.

XX PR 24-APR-1996; 96EP-00201094.

XX PR 24-APR-1996; (UYGR-) RIJKSUNIV GRONINGEN.

XX PI Van Veen HW, Venema K, Bolhuis H, Konings WN;

XX DR WPI; 1997-535844/49.

XX PT Prokaryotic homologue of human multiple drug resistance protein - used to screen for compounds that inhibit, or avoid, drug resistance.

XX CLaim 10; Fig 1; 35PP; English.

XX WPI; 1997-535844/49.

XX PT Prokaryotic homologue of human multiple drug resistance protein - used to screen for compounds that inhibit, or avoid, drug resistance.

XX DR WPI; 1997-535844/49.

CC The present invention describes a recombinant or isolated nucleic acid

CC (1), derived from a prokaryotic gene, which encodes at least a specific CC and/or functional part of transporter protein (TP), or its derivatives, CC which has functional and/or structural similarity with the P-glycoprotein CC (PG) encoded by the human multidrug resistance (MDR) 1 gene. The present CC sequence represents the human MDR1 protein, derived from MDR1-N and MDR1-

CC C as shown in the specification in figure 1. (1) is used to express CC recombinant proteins; its fragments are also useful as probes and primers CC for detection and amplification of related DNA. The protein produced, or CC cells expressing them, are used to determine if substances can inhibit, CC or avoid, MDR proteins, and in a screening method for identifying CC compounds that inhibit transport of cytotoxic substances from cells.

CC Also, cells with a transmembrane protein, especially where expressed from

CC (1), can provide (addititonal) MDR, particularly for use as a model system CC to study mechanisms of action of PG. (Updated on 25-MAR-2003 to correct CC field.)

XX Sequence 1280 AA;

Query Match Score 6218; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

1 MDLEGDRANGGAEEKKKPFCLNNKSKGDKCCKRKPTVSVSMPMRSNWLDKLYMVYGTLLAAI 60
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1 MDLEGDRNGGAKCKCNPFCLNNKSBDKCKCCKRKPTVSVSMPRNSNWLDKLYMVYGTLLAAI 60
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 61 HAGGLPLMLVFSMDMTDFANAGNLGICALLTINNSNTIDTPVNALEDEDMTRAYAASSG 120
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 61 HAGGLPLMLVFSMDMTDFANAGNLGICALLTINNSNTIDTPVNALEDEDMTRAYAASSG 120
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1201 EATSLDTESEKTYOEAALDKAREGRCTCYTAHRLSTIONADLTVFQNGRVKEGHTHQL 1260
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 121 1GAGVLVAYAOVSFWCLIAAGROIHKIKRKOFFAHFIAHQEQIGMFVDVGEATRLLDDVS 180
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 121 1GAGVLVAYAOVSFWCLIAAGROIHKIKRKOFFAHFIAHQEQIGMFVDVGEATRLLDDVS 180
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 181 KINEGICDICKGMFQSMWATPFFCTPIYGTRGKLTIVLAIISPVLGLSAAWAKILSFT 240
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 181 KINEGICDICKGMFQSMWATPFFCTPIYGTRGKLTIVLAIISPVLGLSAAWAKILSFT 240
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 241 DKELLAYKAGAAEELVLAIRTVIAAPGGKKELERYTKNLEEKRKIGKKAITANISIG 300
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 241 DKELLAYKAGAAEELVLAIRTVIAAPGGKKELERYTKNLEEKRKIGKKAITANISIG 300
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 301 AAFLITYASAYALAFAWGTTLVLSKEYSIGQVLTIVPPSTLIGAFSGVGASPSTEAPANARG 360
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 301 AAFLITYASAYALAFAWGTTLVLSKEYSIGQVLTIVPPSTLIGAFSGVGASPSTEAPANARG 360
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 361 AAIFPKIDNKPSIDSYSKSCHKPKDNKKGNELEFRAYVTFSPSRKETVTKLGNLNKVSG 420
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 361 AAIFPKIDNKPSIDSYSKSCHKPKDNKKGNELEFRAYVTFSPSRKETVTKLGNLNKVSG 420
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 421 QTVALYNGGCKSSTTVQLMORLYDPTGMVSYDGDQDRTINTVRLREBIIGYVSQEPVLF 480
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 421 QTVALYNGGCKSSTTVQLMORLYDPTGMVSYDGDQDRTINTVRLREBIIGYVSQEPVLF 480
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 481 ATTAEENRYGRDVDTMDBIEKAVKEANEAYDFTMKLPKFDLIVGERGAOLGGQKORIA 540
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 481 ATTAEENRYGRDVDTMDBIEKAVKEANEAYDFTMKLPKFDLIVGERGAOLGGQKORIA 540
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 541 TARALVNPKILLDEATSALDTESEAUVQVALDKARGKRTTVIAHLSTYRNADVAG 600
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 541 TARALVNPKILLDEATSALDTESEAUVQVALDKARGKRTTVIAHLSTYRNADVAG 600
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 601 FDDGVIVTKGNHDDELMKRGKIGIYPTKLYTMNOTAGNEBIELENDADESKSEDTLEMSSHDGS 660
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 601 FDDGVIVTKGNHDDELMKRGKIGIYPTKLYTMNOTAGNEBIELENDADESKSEDTLEMSSHDGS 660
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 661 SLIRKRSTRSRSVRSQGQDRKLSTKEADIDESIPPSPRIMCLNLNTEPYPTVYGFCAII 720
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 661 SLIRKRSTRSRSVRSQGQDRKLSTKEADIDESIPPSPRIMCLNLNTEPYPTVYGFCAII 720
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 721 NGQIOPAFAVIFSKIGIYPTRNDDAETKRONSNSLFLPPTTGTTFLOGFTFKKA 780
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 721 NGQIOPAFAVIFSKIGIYPTRNDDAETKRONSNSLFLPPTTGTTFLOGFTFKKA 780
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 841 ANLGTGIIISLIYKWLTTLLAAYPIIAIAGVYEMKMSGOALKDKBEGLAGKIAATE 900
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 841 ANLGTGIIISLIYKWLTTLLAAYPIIAIAGVYEMKMSGOALKDKBEGLAGKIAATE 900
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 901 IENFRTVSLSLQEOKFERNYDOSLOVPTVNSLRKAHIGFTPSSTQAMNPFSTAGCFRG 960
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 901 IENFRTVSLSLQEOKFERNYDOSLOVPTVNSLRKAHIGFTPSSTQAMNPFSTAGCFRG 960
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 961 AYLVAHSLMSFEDVTLVFSAVFGAMAQGYSSFAPDVAKAVKSAAHIMIETPLIDS 1020
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 961 AYLVAHSLMSFEDVTLVFSAVFGAMAQGYSSFAPDVAKAVKSAAHIMIETPLIDS 1020
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1021 YSTEGLKPTLEGANTTENYENPTLDPVLCGSLSEYKKGOTLAVGSSCGCKSRTV 1080
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1021 YSTEGLKPTLEGANTTENYENPTLDPVLCGSLSEYKKGOTLAVGSSCGCKSRTV 1080
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1081 QLLERPYDPLAKVLDGKBIKQLNQMLRAHLGTVSQSPILPDCSISERNIAYGDNSSRVV 1140
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1081 QLLERPYDPLAKVLDGKBIKQLNQMLRAHLGTVSQSPILPDCSISERNIAYGDNSSRVV 1140
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1141 SQEEVRAKEANTHAFIBELPNKSTRVGDKGTLQSGQKOKRIARALVRPHILLD 1200
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1141 SQEEVRAKEANTHAFIBELPNKSTRVGDKGTLQSGQKOKRIARALVRPHILLD 1200
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1201 EATSLDTESEKTYOEAALDKAREGRCTCYTAHRLSTIONADLTVFQNGRVKEGHTHQL 1260
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1201 EATSLDTESEKTYOEAALDKAREGRCTCYTAHRLSTIONADLTVFQNGRVKEGHTHQL 1260
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1261 LAQKGYFMSNVSVQGAKHQ 1280
 Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1261 LAQKGYFMSNVSVQGAKHQ 1280
 Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 7
 AAY58186 standard; protein, 1280 AA.
 XX
 ID AAY58186
 XX
 AC AAY58186;
 XX
 DR 14-MAR-2000 (first entry)
 XX
 Human wild-type multidrug resistance-1 (MDR-1) protein.
 DB DE
 XX
 KW Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
 KW haematopoietic stem cell; transduction; bone marrow transplantation;
 KW chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
 KW genetic defect; thalassemia; Gaucher's disease; sickle cell anaemia;
 KW leukaemia; ex vivo expansion; cytokine; wild-type.
 XX
 Homo sapiens.
 OS OS
 XX
 Key Location/Qualifiers
 FT Misc-difference 185
 /note= "This residue is Val in a mutant MDR-1 (AAY58187)".
 XX
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PR 28-MAY-1998;
 XX
 PA W09961589-A2.
 PN PN
 XX
 PD 02-DEC-1999.
 XX
 PP 27-MAY-1999;
 XX
 PR 28-MAY-1998;
 XX
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PR 2000-072615/06.
 DR N-PSDB, AR49332.
 XX
 PT Ex vivo expansion of hematopoietic stem cells transduced with a sequence
 PT encoding human multidrug resistance-1, used for bone marrow
 PT transplantation.
 XX
 PS Claim 10; Page 71-79; 113PP; English.
 XX
 CC This sequence represents human wild-type multidrug resistance protein MDR-1.
 CC MDR-1 is a transmembrane efflux pump, responsible for the export of
 CC drugs from certain cells, particularly cancer cells. Wild-type MDR-1
 CC shows increased resistance to etoposide and decreased resistance to vinca
 CC alkaloids compared with a mutant form (AAY58187) where the Gly at
 CC position 185 is replaced by Val. The invention relates to transducing
 CC haematopoietic stem cells with nucleic acid encoding an MDR protein and
 CC culturing the modified cells. The modified haematopoietic stem cells are
 CC useful in bone marrow transplantation (to reconstitute haematopoietic
 CC systems in patients who have undergone chemotherapy or radiation therapy)
 CC and in ex vivo gene therapy of genetic defects in cells derived from
 CC haematopoietic stem cells, e.g., thalassaemia, Gaucher's disease, sickle
 CC cell anaemia or leukaemia. Modified cells can also be used to
 CC identify factors involved in regulating proliferation and differentiation

Query Match 96.6%; Score 6209; DB 2; Length 1280;
 Best Local Similarity 96.6%; Pred. No. 0; Gaps 0;
 Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGGAEKNNPKLNNKSKDKCERKEPTYSVFSMFRYSNWLDCLMMYVTGLARI 60
 Db 1 MDLEGDRNGGAKCKNPKLNNKSKDKCERKEPTYSVFSMFRYSNWLDCLMMYVTGLARI 60
 Qy 61 HGAGIPPLMVLFGMTDTPANAGNGLDCLALLNSNTDTPVMNLBEDMTRYATTSG 120
 Db 61 HGAGIPPLMVLFGMTDTPANAGNLEDMSNITRSNDTGPMNLBEDMTRYATTSG 120
 Qy 121 IGACTYLVAAYIQSVFWCLAGROTHKIRKOFFHAIIMRQDINGWFDVHDGELENTRLDIVS 180
 Db 121 IGACTYLVAAYIQSVFWCLAGROTHKIRKOFFHAIIMRQDINGWFDVHDGELENTRLDIVS 180
 Qy 181 KINGIGDKGMPFOSMATEPPTGPTIVGTRGMKLTVLTLAISPVGLSAAWAKILSFT 240
 Db 181 KINGIGDKGMPFOSMATEPPTGPTIVGTRGMKLTVLTLAISPVGLSAAWAKILSFT 240
 Qy 241 DKELLAYAKGAAVEVLAIRTYTAFGOKKELEYTNCLEAKIGIKKATANISIG 300
 Db 241 DKELLAYAKGAAVEVLAIRTYTAFGOKKELEYTNCLEAKIGIKKATANISIG 300
 Qy 301 AAFLIYASAYALAFWYGTTLVLSKEYSIGVLTIVSGLAFSVGAAPSIEFANARG 360
 Db 301 AAFLIYASAYALAFWYGTTLVLSKEYSIGVLTIVSGLAFSVGAAPSIEFANARG 360
 Qy 361 AAPELFKIDDNKPSPDSYSKSGHKPDNICKNLLEPNHVFHPSRSKEVVKLGMLNKVQSG 420
 Db 361 AAPELFKIDDNKPSPDSYSKSGHKPDNICKNLLEPNHVFHPSRSKEVVKLGMLNKVQSG 420
 Qy 421 QTVALVGNSGGKSTTVQMLRLDPTEGMYSDQDIRTINVRFLETIGVNSQEPVLF 480
 Db 421 QTVALVGNSGGKSTTVQMLRLDPTEGMYSDQDIRTINVRFLETIGVNSQEPVLF 480
 Qy 481 ATTIAENIRYGREDTMDEIKAVEREANAYDFIMKLQPQEDTLVGERAQOLSGGOKQRIA 540
 Db 481 ATTIAENIRYGREDTMDEIKAVEREANADPIMKLQPQEDTLVGERAQOLSGGOKQRIA 540
 Qy 541 TARALVRNPKILLDEATSADTDSEAVAOVALDKARKEERTTIVIAHRLSTVRADVIAIG 600
 Db 541 TARALVRNPKILLDEATSADTDSEAVAOVALDKARKEERTTIVIAHRLSTVRADVIAIG 600
 Qy 601 PDDGTVVEKENHDELMKEGYKLYMOTAGNEELLENDADESSETDLEMSSHDSGS 660
 Db 601 FDDGTVVEKENHDELMKEGYKLYMOTAGNEYELLENDADESSETDLEMSSHDSGS 660
 Qy 661 SLRKRSSTRSVRGSGQDRKLSTREALDESIPPYSWRIMKLNTTEMPLPVVGYPCAI 720
 Db 661 SLRKRSSTRSVRGSGQDRKLSTREALDESIPPYSWRIMKLNTTEMPLPVVGYPCAI 720
 Qy 721 NGGLOPAFVIFSKLIGLFTNDDAETKRONSNLFLLFLVGLIVSFITPFLQGTTGKA 780
 Db 721 NGGLOPAFVIFSKLIGLFTNDDAETKRONSNLFLLFLVGLIVSFITPFLQGTTGKA 780
 Qy 781 GEILTRLRYVERSURQDODPDKNTGALITRLANDAAQTKAIGSRLATQNI 840
 Db 781 GEILTRLRYVERSURQDODPDKNTGALITRLANDAAQTKAIGSRLATQNI 840
 Qy 841 ANLGIIISLYGWOTLILIAVPIIALGVEMKMLSCORLKDKELEGAGCIATEA 900
 Db 841 ANLGIIISLYGWOTLILIAVPIIALGVEMKMLSCORLKDKELEGAGCIATEA 900
 Qy 901 IENFRIVTWSLQOBKEPHMTDQSLOVYPRNSLRKAHFGTTSPTOMMFSYACCRFG 960
 Db 901 IENFRIVTWSLQOBKEPHMTDQSLOVYPRNSLRKAHFGTTSPTOMMFSYACCRFG 960
 Qy 961 AYLVHSMSDVLVFSAVYFGANAVGOVSFADYAKVSAHIMIETPLIDS 1020
 Db 961 AYLVHSMSDVLVFSAVYFGANAVGOVSFADYAKVSAHIMIETPLIDS 1020
 Qy 1021 YSTEGLKPNTILEGNUTPEVVFNYPTLDIPVLOGLSLEVKGQTIALVGSGGKSTVV 1080

Db 1021 YSTEGLKPNTILEGNUTPEVVFNYPTLDIPVLOGLSLEVKGQTIALVGSGGKSTVV 1080
 Qy 1081 QLLERFDPLAGKVLDGKEIKQNLQYQWLSLEYKGQTIALVGSGGKSTVV 1140
 Db 1081 QLLERFDPLAGKVLDGKEIKQNLQYQWLSLEYKGQTIALVGSGGKSTVV 1140
 Qy 1141 SOEIVRAKEANAHAFIESLPNKYSYTRVGDKGTLQSGGOKRIATRALYPROPHILLD 1200
 Db 1141 SOEIVRAKEANAHAFIESLPNKYSYTRVGDKGTLQSGGOKRIATRALYPROPHILLD 1200
 Qy 1201 EATSALDTESEKVVQBALDKAREGRTCIVIAHLSTIONALIVVONGRYKEGHTHQL 1260
 Db 1201 EATSALDTESEKVVQBALDKAREGRTCIVIAHLSTIONALIVVONGRYKEGHTHQL 1260
 Qy 1261 LAQGIYFSMVSYQAGKQ 1280
 Db 1261 LAQGIYFSMVSYQAGKQ 1280

RESULT 11
 US-09-817-762-3 ; Sequence 3 , Application US/098117762
 Parent No. 6886774 ;
 GENERAL INFORMATION:
 ; APPLICANT: Spalding, Edgar P.;
 ; INVENTOR: No. 6886774, Bosi
 ; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 13328-00061
 ; CURRENT APPLICATION NUMBER: US/09/817,762
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIORITY NUMBER: PCT/US99/22363
 ; PRIORITY FILING DATE: 1999-09-24
 ; PRIORITY APPLICATION NUMBER: US 60/101,814
 ; PRIORITY FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PasteSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1,280
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; DATABASE ACCESSION NUMBER: Genbank P08183
 ; DATABASE ENTRY DATE: 1997-11-01
 US-09-817-762-3

Query Match 96.6%; Score 6209; DB 2; Length 1280;
 Best Local Similarity 96.6%; Pred. No. 0; Mismatches 25; Indels 0; Gaps 0;
 Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGGAEKNNPKLNNKSKDKCERKEPTYSVFSMFRYSNWLDCLMMYVTGLARI 60
 Db 1 MDLEGDRNGGAKCKNPKLNNKSKDKCERKEPTYSVFSMFRYSNWLDCLMMYVTGLARI 60
 Qy 121 IGAQTYVAAQYQSVFWCLAGROTHKIRKOFFHAIIMRQDINGWFDVHDGELENTRLDIVS 180
 Db 121 IGAQTYVAAQYQSVFWCLAGROTHKIRKOFFHAIIMRQDINGWFDVHDGELENTRLDIVS 180
 Qy 1261 KINBTIGDKGMPFOSMATEPPTGPTIVGTRGMKLTVLTLAISPVGLSAAWAKILSFT 240
 Db 1261 KINBTIGDKGMPFOSMATEPPTGPTIVGTRGMKLTVLTLAISPVGLSAAWAKILSFT 240
 Qy 1301 DKELLAYAKGAAVEVLAIRTYTAFGOKKELEYTNCLEAKIGIKKATANISIG 300
 Db 1301 DKELLAYAKGAAVEVLAIRTYTAFGOKKELEYTNCLEAKIGIKKATANISIG 300

FILING DATE: 22-MAY-1992
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1260 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 US - 08-583-276-19

	Query	Match	Score	DB 1:	Length
Db	721 NGGLQPAFAITISKIGVYTRIDDPETRQNNSNLFSLPLAIGIISITFFLQGFTGKA	780	96.6%	6206;	1280;
Qy	781 GEILTKRLRYMERSMLRDVSFWDPPNTGALTTLANDAAQVKAIGSPLAITQNI	840	96.5%	Pred. No. 0;	
Db	781 GEILTKRLRYMERSMLRDVSFWDPPNTGALTTLANDAAQVKAIGSRLAVITQNI	840	96.5%	Mismatches 20;	
Qy	841 ANLGTGIIISIISIYGWQTLLLIAIVPIIAIAGVEMKLSQALDKKKELEGAGKATEA	900	96.5%	Indels 0;	Gaps 0;
Db	841 ANLGTGIIISIISIYGWQTLLLIAIVPIIAIAGVEMKLSQALDKKKELEGAGKATEA	900	96.5%		
Qy	901 IENPRTVSLTQDQKPEHMTDOSLOVEYRNSLRKAIHFGITPSPTOAMMFSYACGFRFG	960	96.5%		
Db	901 IENPRTVSLTQDQKPEHMTDOSLOVEYRNSLRKAIHFGITPSPTOAMMFSYACGFRFG	960	96.5%		
Qy	961 AYLVAHSLMSPDVLLVFSAVVFGAMAQVSSFPADYAKAVSAAHHTIMIEKTPPLIDS	1020	96.5%		
Db	961 AYLVAHKLMSPDVLLVFSAVVFGAMAQVSSFPADYAKAVSAAHHTIMIEKTPPLIDS	1020	96.5%		
Qy	1021 YSTEGLKPKNTLEGNFTNEVVFNYPTRLDPVLOCISLSEVKKGOTPLAVGSSGGKSTTV	1080	96.5%		
Db	1021 YSTEGLKPKNTLEGNFTNEVVFNYPTRLDPVLOCISLSEVKKGOTPLAVGSSGGKSTTV	1080	96.5%		
Qy	1081 QLLERFYDPLAGKVLLDGEIKIKQLNQWTRAHLGIVSQBPLFDCSISENIAYEDNSRVV	1140	96.5%		
Db	1081 QLLERFYDPLAGKVLLDGEIKIKQLNQWTRAHLGIVSQBPLFDCSISENIAYEDNSRVV	1140	96.5%		
Qy	1141 SOBEVTRRAKEANIAHFISSLPNCKSTRVGDKGTLQSGKQRIATAARALVROPHILLID	1200	96.5%		
Db	1141 SOBEVTRRAKEANIAHFISSLPNCKSTRVGDKGTLQSGKQRIATAARALVROPHILLID	1200	96.5%		
Qy	1201 EATSLADTSESEKVKYORALDKAREERTCTVIAHRLSTIONADLIVFQNGRVEKHGTQQL	1260	96.5%		
Db	1201 EATSLADTSESEKVKYORALDKAREERTCTVIAHRLSTIONADLIVFQNGRVEKHGTQQL	1260	96.5%		
Qy	1261 LAOKGIYFSMVSVOGAKRQ	1280	96.5%		
Db	1261 LAOKGIYFSMVSVOGAKRQ	1280	96.5%		
RESULT 13 US-08-583-276-19 Sequence 19, Application US/08583276					
GENERAL INFORMATION:					
APPLICANT:	McDonagh, Kevin T.				
APPLICANT:	Nienhuis, Arthur				
APPLICANT:	Tolesoshev, Paul				
TITLE OF INVENTION:	IMPROVED EXPRESSION OF HUMAN				
TITLE OF INVENTION:	MULTIDRUG RESISTANCE GENES AND IMPROVED				
TITLE OF INVENTION:	SELECTION OF CELLS TRANSDUCED WITH SUCH GENES				
NUMBER OF SEQUENCES:	19				
CORRESPONDENCE ADDRESS:	Carroll, Byrne, Bain, Gilfillan,				
ADDRESSSEE:	Cecchi & Stewart				
STREET:	6 Becker Farm Road				
CITY:	Roseland				
STATE:	New Jersey				
ZIP:	07068				
COMPUTER READABLE FORM:					
MEDIUM TYPE:	3.5 inch diskette				
COMPUTER:	IBM PS/2				
OPERATING SYSTEM:	PC-DOS				
SOFTWARE:	DNA V2				
CURRENT APPLICATION DATA:					
APPLICATION NUMBER:	US/08/583,276				
FILING DATE:	05-JAN-1996				
CLASSIFICATION:	435				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	08/332,444				
FILING DATE:	31-OCT-1994				
APPLICATION NUMBER:	07/887,712				

841	ANLGTGIIISPIYGKQFQLTLLIAIVPIIAJGVYEMKMLSGQALDKKELEGAGKIAATE	900
901	TENFTTVSLTQEQRPERMYDOSLOVTPNSLRKAHIFGTTSPSTQAMMFYSAVGCPRFG	960
901	TENFTTVSLTQEQRPERMYAQSLOVTPNSLRKAHIFGTTSPSTQAMMFYSAVGCPRFG	960
961	AYLVAHKLMSFEDVILVPSAVYFGAMAVGQSYSSAPDYAKYSAHIMITEKTPPLIDS	102
961	AYLVAHKLMSFEDVILVPSAVYFGAMAVGQSYSSAPDYAKYSAHIMITEKTPPLIDS	102
1021	YSTEGIKKPNTLEGNVTNSVVFNYPTRLDIPVLCQSLTEVKKGCTTLALVGSSCGKSVY	108
1021	YSTEGIKKPNTLEGNVTNSVVFNYPTRLDIPVLCQSLTEVKKGCTTLALVGSSCGKSVY	108
1081	QLEREYDPLAKVLDLGKEIKOLNQVMIRAHGIVSQBPLPQCSISENIAGNDNSRVV	114
1081	QLEREYDPLAKVLDLGKEIKOLNQVMIRAHGIVSQBPLPQCSISENIAGNDNSRVV	114
1141	SQEETYRAAEKANTIAFIESLPNKYSTRVGDKGTOLGSGKOKRATAARALVRPHILLID	120
1141	SQEETYRAAEKANTIAFIESLPNKYSTRVGDKGTOLGSGKOKRATAARALVRPHILLID	120
1201	BATSAALDESEKVQBALDKAREGRCTCIVAHRLSTIONADLITYFONGRCVEGHGTHOOL	126
1201	BATSAALDESEKVQBALDKAREGRCTCIVAHRLSTIONADLITYFONGRCVEGHGTHOOL	126
1261	LAQKGIYFSMYSVQAGAKRO 1280	
1261	LAQKGIYFSMYSVQAGAKRO 1280	
RESULT 14		
5206352-4		
	; Patent No. 5206352	
	; APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,	
	; Michael M.	
	; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA	
	; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS	
	; NUMBER OF SEQUENCES: 4	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/07/622, 836	
	; FILING DATE: 24-SEP-1990	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: 892, 575	
	; FILING DATE: 01-AUG-1986	
	; APPLICATION NUMBER: 845, 610	
	; FILING DATE: 28-MAR-1986	
	; SEQ ID NO:4;	
	5206352-4	
Qy	Query Match 96.6%; Score 6206; DB 7; Length 1280;	
	Best Local Similarity 96.5%; Pred. No. 0; Mismatches 25; Indels 0; Gaps 0	
Matches 1235; Conservative		
Db	1 MDLEGDDNGGALKNPFLNNKSKDCKKEKPTVSPSMRYSWLDKLYMVGTAAII 60	
	1 MDLEGDDNGGALKNPFLNNKSKDCKKEKPTVSPSMRYSWLDKLYMVGTAAII 60	
Qy	1 HGAIGPLPMLYFGDMTDIFANAGNLGPGLALITNSNITDVPVNLBDMTRAYTSG	120
Db	61 HGAIGPLPMLYFGDMTDIFANAGNLGPGLALITNSNITDVPVNLBDMTRAYTSG	120
Qy	121 TCAAGVLVAAYIYQSPWCLAAQRQHMKURKQFFHAIRMQRGWFDVHDYGELENTRDDVS	180
Db	121 TCAAGVLVAAYIYQSPWCLAAQRQHMKURKQFFHAIRMQRGWFDVHDYGELENTRDDVS	180
Qy	121 TCAAGVLVAAYIYQSPWCLAAQRQHMKURKQFFHAIRMQRGWFDVHDYGELENTRDDVS	180
Db	121 TCAAGVLVAAYIYQSPWCLAAQRQHMKURKQFFHAIRMQRGWFDVHDYGELENTRDDVS	180
Qy	181 KINEGICDKIGMFQSMATPFTGIVPGTRGKLTIVIALISPGLSAAWAKILSSFT	241
Db	181 KINEGICDKIGMFQSMATPFTGIVPGTRGKLTIVIALISPGLSAAWAKILSSFT	241
Qy	181 KINQVIGDKIGNPQSMATPFTGIVPGTRGKLTIVIALISPGLSAAWAKILSSFT	241
Db	181 KINQVIGDKIGNPQSMATPFTGIVPGTRGKLTIVIALISPGLSAAWAKILSSFT	241
Qy	241 DKSLVATAKAGAYAEEAYLAARTVIAFGQKRELYNKDNEARIGRKATAANISG	300

241	DKELLIYAKAGAVERLAIRTYTAFGGKKKEFRYNKLEEARIGIKKATAANISIG	300
301	AAFLIYASALAFYGTTLVLSKREYSIGOVLTVPSVLIGAVSQAPSIEARANARG	360
301	AAFLIYASALAFYGTTLVLSKREYSIGOVLTVPSVLIGAVSQAPSIEARANARG	360
361	AAPEFIKTIIDNKPSDSYSIGSHKDNNIKNLNEFFANHVFYPSRECEVKILKGLNJKVQSG	420
361	AAVEPKIIDNKPSDSYSIGSHKDNNIKNLNEFFANHVFYPSRECEVKILKGLNJKVQSG	420
421	QTVALVGNSCGKSITVQLMQLRYPTEGVNSVDQDIRTINVRPLRE11GIVSQEPVLF	480
421	QTVALVGNSCGKSITVQLMQLRYPTEGVNSVDQDIRTINVRPLRE11GIVSQEPVLF	480
481	ATTIAENIYRGEDVTMDELEKAVENTANAYDFIMLPLQKEDTLYCERGAOLSGGGKQKRIA	540
481	ATTIAENIYRGENTMDELEKAVENTANAYDFIMLPLKEDTLYCERGAOLSGGGKQKRIA	540
541	TARALYRNPKLILDEATSAALSALDTESEAVVOVALDARKKGTTIVAHRLSTVRNDVIAG	600
541	TARALYRNPKLILDEATSAALSALDTESEAVVOVALDARKKGTTIVAHRLSTVRNDVIAG	600
601	FDDGIVTKENHDELMKKGKYPKLVMTAGNEELENADESKSEIDTLEMSSHDSGS	660
601	FDDGIVTKENHDELMKKGKYPKLVMTAGNEELENADESKSEIDTLEMSSHDSGS	660
661	SURKRSTRSVRGSOCDRKLSITGEALDESIPPSWRTMLKLNTJEWPYFVVGFCALL	720
661	SURKRSTRSVRGSOCDRKLSITGEALDESIPPSWRTMLKLNTJEWPYFVVGFCALL	720
721	NGCLQPAFAVIFSKIGIPTNDAAETKRONSLTLLFLFLVLTGITSFIRTPFLQGFTGKA	780
721	NGCLQPAFAVIFSKIGVFTTIDDPKTKRQNSNLSSFLFLAUGISFIRTPFLQGFTGKA	780
781	GELLTKRLYMPRSMLRDQYSWPDPKNTTGALTTRLANDAAQYKGAIGSRLLATTONI	840
781	GELLTKRLYMPRSMLRDQYSWPDPKNTTGALTTRLANDAAQYKGAIGSRLLATTONI	840
841	ANTGTGIIISLYGWQITLLIAIVPITIAAGVVMKMSQALIDKCKCELEGAGKIAATE	900
841	ANTGTGIIISLYGWQITLLIAIVPITIAAGVVMKMSQALIDKCKCELEGAGKIAATE	900
901	IENPRITYSLTQEQQKPHMYIQSLQPYRNSLRKAHIFGTFSTQAMMFSYAGCPFRG	960
901	IENPRITYSLTQEQQKPHMYIQSLQPYRNSLRKAHIFGTFSTQAMMFSYAGCPFRG	960
961	AIVLAHSILMSFDVLLVSAVFGAVAVGQISSPADDYAKKVSAAHTIMIIEKTPLIDS	1024
961	AIVLAHKLMSFDVLLVSAVFGAVAVGQISSPADDYAKKVSAAHTIMIIEKTPLIDS	1024
1021	YSTEGNLKENTLEGNTNEWVNYFTRDIPLYQGISLEVKGKQTLAVGSSGCKSTVV	1088
1021	YSTEGNLKENTLEGNTNEWVNTFGEVNVYFTRDIPLYQGISLEVKGKQTLAVGSSGCKSTVV	1088
1081	OLLERYFDPLAGKVLQCKEIQNLQNYOWRAHLGIVSQEPILFDCTSSENAYGDSRSVV	1144
1081	OLLERYFDPLAGKVLQCKEIQNLQNYOWRAHLGIVSQEPILFDCTSSENAYGDSRSVV	1144
1144	SOBIVRAKEANIHAFESL彭KYSFRVGDGTOLSGGOKORIAJARALYRPHILLD	1200
1144	SQEIVRAKEANIHAFESL彭KYSFRVGDGTOLSGGOKORIAJARALYRPHILLD	1200
1201	RATSALDTESEKVYQEALDKAREGRTCLVIAIRLSTIONALIVFONGRYKEGHGTHQQL	126
1201	EATSLDTESEKVYQEALDKAREGRTCLVIAIRLSTIONALIVFONGRYKEGHGTHQQL	126
1261	LAQGIYFSMSVYQAGAQHQ	1280
1261	LAQGIYFSMSVYQAGTRHQ	1280

1 MDLEGDRNGGAEKKNPFPKLANKSKDKKERRKPTVSYFSMFRYSNVLKLYMVVGTLAAII 60
 1 MDLEGDRNGGAEKKNPFPKLANKSKDKKERRKPTVSYFSMFRYSNVLKLYMVVGTLAAII 60
 61 HGAGLPLMMVFGDMTDTPANAGNIGDGLALL--TNSNNITDTYPVMMLEEDMTRYATTY 117
 61 HGAGLPLMMVFGDMTDTPANAGNIGDGLALLFANNNSNITDTYPVMMLEEDMTRYATTY 120
 118 YSGIGGVLYAYIQSFWCLAAGRQHKRKQKPFHAIRMROBIGHFDYGEILNTRLTD 177
 121 YSGIGGVLYAYIOVSFWCLAAGRQHKRKQKPFHAIRMROBIGHFDYGEILNTRLTD 180
 178 DVSXKINGBGDKIGMFQSMATFFPTCPVIGPTRGWKLTVLIAISPVLGSAAVAKILS 237
 181 DVSXKINGBGDKIGMFQSMATFFPTCPVIGPTRGWKLTVLIAISPVLGSAAVAKILS 240
 238 SPTDKELLAYAKAGAYAEEVLAIRTYIAFGQKKELETRKNLBEAKRGIKKITANI 297
 241 SPTDKELLAYAKAGAYAEEVLAIRTYIAFGQKKELETRKNLBEAKRGIKKITANI 300
 298 SIGAFLIIVASYALAFWYGTTLVLSKEYSIGQVLTFFFSTLVGASVGQOASPSIBAFAN 357
 301 SIGAFLIIVASYALAFWYGTTLVLSKEYSIGQVLTFFFSTLVGASVGQOASPSIBAFAN 360
 358 ARGAAEPIKCIDNKSIDSYSKSGHCPDNIGKGNLBRPNVHFSYSPRKEVKILKGNLKV 417
 361 ARGAAEPIKCIDNKSIDSYSKSGHCPDNIGKGNLBRPNVHFSYSPRKEVKILKGNLKV 420
 418 QSGQTVALVGNSGCGKSTTVQLMQLRVDPTEGMSVGDQDIRTRNPRBLIGVSQEP 477
 421 QSGQTVALVGNSGCGKSTTVQLMQLRVDPTEGMSVGDQDIRTRNPRBLIGVSQEP 480
 478 VLFAATTAAENRYGREDTVMDIEKAKEYANADYDFMLKLPQFDIVYGERAQOLSGQKQ 537
 481 VLFAATTAAENRYGREDTVMDIEKAKEYANADYDFMLKLPQFDIVYGERAQOLSGQKQ 540
 538 RIAIARALVRNPKILLDRATSALDTSBAAVQUALDKARKRGTIVIAHRLSTVNADV 597
 541 RIAIARALVRNPKILLDRATSALDTSBAAVQUALDKARKRGTIVIAHRLSTVNADV 600
 598 IAGFDGTVIYEGNHDELMKKGIFYFLVMTAGNEIELNAADESKSEIDTLLENSSHD 657
 601 IAGFDGTVIYEGNHDELMKKGIFYFLVMTAGNEIELNAADESKSEIDTLLENSSHD 660
 658 SGSSLIKRSTRSRVSQSQDKLKSTEALDESIPPSFWMIUMNLTETPYFVGWFC 717
 661 SGSSLIKRSTRSRVSQSQDKLKSTEALDESIPPSFWMIUMNLTETPYFVGWFC 720
 718 ALINGQLOPAFAVFSKIGIFTRNDDETKRONSNLFLVLGIVSPTTFLOGFTF 777
 721 ALINGQLOPAFAVFSKIGIFTRNDDETKRONSNLFLVLGIVSPTTFLOGFTF 780
 778 KGAEILTKRLYMFRSMLRQDWSWPDPKNTGALTTRLANDAQYKGAGSRRAIT 837
 781 GRAGEILTKRLYMFRSMLRQDWSWPDPKNTGALTTRLANDAQYKGAGSRRAIT 840
 838 QNTANLGRGITSLIYRQFLTLLAIVPIIAJAGVVERMUSQQLDKCELEGACKIA 897
 841 QNTANLGRGITSLIYRQFLTLLAIVPIIAJAGVVERMUSQQLDKCELEGACKIA 900
 898 TEAIENPFTVYSLTQEOKPEFRMDQSLQPYRNRSRKAHIFGITSFQAMMFSAGCP 957
 901 TEAIENPFTVYSLTQEOKPEFRMDQSLQPYRNRSRKAHIFGITSFQAMMFSAGCP 960
 958 RFGAYLYAHSLMSPEDVYLVSAYVFGAMAVGQVSFAPPDYAKAVKSAAHIMIETKPL 1017
 961 RFGAYLYAHSLMSPEDVYLVSAYVFGAMAVGQVSFAPPDYAKAVKSAAHIMIETKPL 1020
 1018 IDSYSTEGLPKPNLLEGAVTNEVTPNTPRLDPLVQCLSLSLTKKGQTLAIVGSSGCKS 1077
 1021 IDSYSTEGLPKPNLLEGAVTNEVTPNTPRLDPLVQCLSLSLTKKGQTLAIVGSSGCKS 1080
 1078 TVVQLLERFYDPLAKVLLDGKRIQKLNQVWLAHLGIVSQBPLFDCSISENIAYGDNS 1137

Db 1081 TVVQLLERFYDPLAKVLLDGKRIQKLNQVWLAHLGIVSQBPLFDCSISENIAYGDNS 1140
 Db 1138 RVSQEBETVRAAEKANTHAFIESLPNKYSTRVGDKGTLQSGGGKQRATAIALVQRPHL 1197
 Qy 1141 RVSQEBETVRAAEKANTHAFIESLPNKYSTRVGDKGTLQSGGGKQRATAIALVQRPHL 1200
 Qy 1198 LDDEATSALDTSSEKVOAELDKAREGTCIVIAHRLSTIONADLIVVQNGRKVEKHGTH 1257
 Db 1201 LDDEATSALDTSSEKVOAELDKAREGTCIVIAHRLSTIONADLIVVQNGRKVEKHGTH 1260
 Qy 1258 QLLAQKGIFYFSMVSVOAGAKRQ 1280
 Db 1261 QLLAQKGIFYFSMVSVOAGAKRQ 1283

RESULT 6
 Sequence 2, Application US/09584586
 Patient No. 6933-50

GENERAL INFORMATION:
 APPLICANT: Sorrentino, Brian
 APPLICANT: Bunting, Kevin
 TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 FILE REFERENCE NUMBER: US/09/584,586
 CURRENT APPLICATION NUMBER: US/09/584,586
 CURRENT FILING DATE: 2000-05-31
 EARLIER APPLICATION NUMBER: US 60/086,988
 EARLIER FILING DATE: 1998-05-28
 EARLIER APPLICATION NUMBER: PCT/US99/11825
 EARLIER FILING DATE: 1999-05-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patentin Ver. 2.0
 LENGTH: 12800
 SEQ ID NO 2
 TYPE: PRT
 ORGANISM: Homo sapiens
 PEGABE: Human MDR 185-G
 OTHER INFORMATION: Human MDR 185-G
 US-09-584-586-2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
 Best Local Similarity 96.6%; Fred. No. 0; Mismatches 24; Indels 0; Gaps 0;
 Matches 1237; Conservative 19; SEQ ID NO 2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
 Best Local Similarity 96.6%; Fred. No. 0; Mismatches 24; Indels 0; Gaps 0;
 Matches 1237; Conservative 19; SEQ ID NO 2

Qy 1 MLEGDRNGGAKKFQPKLANKSKDKKERRKPTVSYFSMFRYSNVLKLYMVGTLLAAII 60
 Db 1 MLEGDRNGGAKKFQPKLANKSKDKKERRKPTVSYFSMFRYSNVLKLYMVGTLLAAII 60
 Qy 61 HGAGLPLMMIYFGDMTDTFANAQNGLDGLALLTNSNNITDTPVPLNLEEDMTRKAYYYSG 120
 Db 61 HGAGLPLMMIYFGDMTDTFANAQNGLDGLALLTNSNNITDTPVPLNLEEDMTRKAYYYSG 120
 Qy 121 IAGFLYAAVQYQSVFCLAGRQHKIRKOFFHAIRMROEIGFWDFVHLNTRLDDVS 180
 Db 121 IAGFLYAAVQYQSVFCLAGRQHKIRKOFFHAIRMROEIGFWDFVHLNTRLDDVS 180
 Qy 1241 KINEGIGDKIIMFFQSMATPTTGFIVGFTGRWKITLVLIAISPVGLSAVWAKLSSFT 240
 Db 1241 DKELLAYAKAGVAEVLLAARTVIAFGGOKKELERYNKKLEAKRIGKKAITANISIG 300
 Qy 1241 KINEGIGDKIIMFFQSMATPTTGFIVGFTGRWKITLVLIAISPVGLSAVWAKLSSFT 240
 Db 1241 KINEGIGDKIIMFFQSMATPTTGFIVGFTGRWKITLVLIAISPVGLSAVWAKLSSFT 240
 Qy 1301 AFLLIYAYAALAFYGTTLVLSKEYSIGVLTFFSVLIGAFSGQAPSIEFAPANG 360
 Db 1301 AFLLIYAYAALAFYGTTLVLSKEYSIGVLTFFSVLIGAFSGQAPSIEFAPANG 360
 Qy 1361 APEFIKIIDNKPIDSYSKSGHCPDNIKENIJEPRNVHFSPRSKVKLKGMLNKVQSG 420
 Db 1361 APEFIKIIDNKPIDSYSKSGHCPDNIKENIJEPRNVHFSPRSKVKLKGMLNKVQSG 420
 Qy 1361 AYEIPIKIIDNKPIDSYSKSGHCPDNIKENIJEPRNVHFSPRSKVKLKGMLNKVQSG 420

FILE REFERENCE: 015280-402100US
 CURRENT APPLICATION NUMBER: US/09/767,594
 CURRENT FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: US 60/177,410
 PRIOR FILING DATE: 2000-01-20
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human P-glycoprotein (Pgp) / multi-drug resistance 1
 OTHER INFORMATION: (Mar-1) ABC transporter (ABC transport)
 OTHER INFORMATION: protein
 US-09-767-594-2

Query	Match	Score	DB	Length
QY	Best Local Similarity	96.6%	2	Length 1280;
Db	Matches 1236; Conservative	96.6%	0;	Pred. No. 0;
QY	Qy	1	MDLEGDRNGGAEKKNPKFLNNNSKKDKKKERKEPTVSYSMFRYSNWLDPKLMLVGTLLAII 60	
Db	Db	1	MDLEGDRNGGAKKKNPKFLNNNSKKDKKKERKEPTVSYSMFRYSNWLDPKLMLVGTLLAII 60	
QY	Qy	61	HGAGLPLMLVIGDMTDIFANGNLIGALITNSNNITDTPVNLLEDMTRAYYYSG 120	
Db	Db	61	HGAGLPLMLVIGDMTDIFANGNLIEDLMSNTNRSIDNDTCFFNNILEDTRAYYYSG 120	
QY	Qy	121	IGAGLVVAYAIQVSFWCLAEGQIKIKRQFFHAIRQEIGMFDADVGELNRLTDVS 180	
Db	Db	121	IGAGLVVAYAIQVSFWCLAGQIKIKRQFFHAIRQEIGMFDADVGELNRLTDVS 180	
QY	Qy	181	KINGIGDKGKIGMFQSNTATPFTGFIVGFTGRKLTLVLAISPVLGJSAAWAKIISST 240	
Db	Db	181	KINEVIGKIGMFQSNTATPFTGFIVGFTGRKLTLVLAISPVLGJSAAWAKIISST 240	
QY	Qy	241	DKEILAYAKAGAAEVLLAATRTVIAFGGOKKELERYNKNLFEAKRGIKKAITANISIG 300	
Db	Db	241	DKEILAYAKAGAAEVLLAATRTVIAFGGOKKELERYNKNLFEAKRGIKKAITANISIG 300	
QY	Qy	301	AATLIVIAYALAAFWYGTLLVLSKEYSIGQVLTFSVLAGFSGDASPTEAFANARG 360	
Db	Db	301	AATLIVIAYALAAFWYGTLLVLSKEYSIGQVLTFSVLAGFSGDASPTEAFANARG 360	
QY	Qy	361	AAPEIFKIDNKEPSIDSYSKGHKPDNIGKNUFRVHFSYSRKVNKILKLNLYKQSG 420	
Db	Db	361	AAPEIFKIDNKEPSIDSYSKGHKPDNIGKNUFRVHFSYSRKVNKILKLNLYKQSG 420	
QY	Qy	421	QTVALVGENSGCCKSSTTYVOLMORLXDPTEGMYSVDGQDIRTINVRFLRIBLGVVSQEPLF 480	
Db	Db	421	QTVALVGENSGCCKSSTTYVOLMORLXDPTEGMYSVDGQDIRTINVRFLRIBLGVVSQEPLF 480	
QY	Qy	481	ATTAAENTRYGREDDYTMDBIEKAVKEANAYDFTMKLPOKFDTLVRGERGAOLSGGKORIA 540	
Db	Db	481	ATTAAENTRYGREDDYTMDBIEKAVKEANAYDFTMKLPHKFDTLVRGERGAOLSGGKORIA 540	
QY	Qy	541	TARALVRAPKILLDEATSALDTESEAIVQVALDKARKGRRTIVIAHRLSTVRNADVIAG 600	
Db	Db	541	TARALVRAPKILLDEATSALDTESEAIVQVALDKARKGRRTIVIAHRLSTVRNADVIAG 600	
QY	Qy	601	FDDGIVIVEKGKGNHDLMKEKG1YFKLVTMQTAGNEIELNAADESKSEIDTLEMSSHSGS 660	
Db	Db	601	FDDGIVIVEKGKGNHDLMKEKG1YFKLVTMQTAGNEIELNAADESKSEIDTLEMSSHSGS 660	
QY	Qy	661	SILRKRSSTRSRVGSOGODRKLSKTEALDESIPPSWRLMCLNLTBMPYFVGVFCAI 720	
Db	Db	661	SILRKRSSTRSRVGSQADRKLSKTEALDESIPPSWRLMCLNLTBMPYFVGVFCAI 720	
QY	Qy	721	NGGQPAVAFVFSKIIIGFTRNDDAETKRQNSNLFSLLFLVYGVISPTFFLOGFTFGKA 780	
Db	Db	721	NGGQPAVAFVFSKIIIGFTRNDDAETKRQNSNLFSLLFLVYGVISPTFFLOGFTFGKA 780	
RESULT	7			
US-09-767-594-2				
i Sequence	2,	Application	US/09767594	
i Patent No.	6521635			
GENERAL INFORMATION:				
APPLICANT: Bates, Susan				
APPLICANT: Robey, Robert				
APPLICANT: The Government of the United States of America				
APPLICANT: as represented by the Secretary of the				
APPLICANT: Department of Health and Human Services				
TITLE OF INVENTION: Inhibition of MDR Transport by Acridine Derivatives				

Qy	1141	SOEETVRAKEANTHAFIESLPLNKYSTKVGDKGTLQSGGKQRKIAJARALVRPHILLID	1200
Db	1141	SQEETVRAKEANTHAFIESLPLNKYSTKVGDKGTLQSGGKQRKIAJARALVRPHILLID	1200
Qy	1201	EATSLADTESEKTYOAEALDKAREGRTCTVIARLSTITQADLIVTFQNGRVEKGTHQOL	1260
Db	1201	EATSLADTESEKTYOAEALDKAREGRTCTVIARLSTITQADLIVTFQNGRVEKGTHQOL	1260
Qy	1261	LAQKGIIYPSMVSVOAGTTRQ	1280
Db	1261	LAQKGIIYPSMVSVOAGTTRQ	1280
RESULT 4			
US-10-101-433A-5			
	Sequence 5, Application US/10101433A		
	Patent No. 6855812		
	GENERAL INFORMATION:		
	APPLICANT: Hanscom, Sara		
	APPLICANT: Crespi, Charles		
	TITLE OF INVENTION: P GLYCOPROTEINS AND USES THEREOF		
	FILE REFERENCE: G00307/70019		
	CURRENT APPLICATION NUMBER: US/10/101, 433A		
	CURRENT FILING DATE: 2002-03-19		
	PRIOR APPLICATION NUMBER: US 60/277, 095		
	PRIOR FILING DATE: 2001-03-19		
	NUMBER OF SEQ ID NOS: 38		
	SOFTWARE: Patentin version 3.0		
	SEQ ID NO 5		
	LENGTH: 1280		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
US-10-101-433A-5			
Query	Match	Score	Length
	Best Local Similarity	6431;	1280;
	Matches 1280;	Pred. No. 0;	
	Conservative	Mismatches	0;
		Indels	Gaps
Y	1 MDLEGDGNGGAKCKCNFPLANKNSKEDKCKBKKCPYTSVPMFRYSNWLQLYMMVTGLAAII	60	0;
b	1 HGAGLPIMLLYFGEMTIDIPAGAGNLEDLSMSNTIINRSINDTGFRMNEDMDTRYAYTYSG	120	
b	1 MDLEGDGNGGAKCKCNFPLANKNSKEDKCKBKKCPYTSVPMFRYSNWLQLYMMVTGLAAII	60	
Y	121 IGAGTVVAYI QVSFNLCAAQROIHKRKFPHATIMQEIGWDFDNGCENTRLTDVS	180	
b	121 IGRGYLVAAVQIVSFCLAAQROIHKRKFPHATIMQEIGWDFDNGCENTRLTDVS	180	
b	121 HGAGLPIMLLYFGEMTIDIPAGAGNLEDLSMSNTIINRSINDTGFRMNEDMDTRYAYTYSG	120	
Y	181 KINEVIGDKIGMFMPSMATPTGPFVQFTCKWLTVVLLASPVGLSAAWVKILSST	240	
b	181 KINEVIGDKIGMFMPSMATPTGPFVQFTCKWLTVVLLASPVGLSAAWVKILSST	240	
b	181 KINEVIGDKIGMFMPSMATPTGPFVQFTCKWLTVVLLASPVGLSAAWVKILSST	240	
/	241 DKEILAYAKAGVAEEVLLAIRTVIAGGOKKELRYNKOLEAERGIKKAITANISIG	300	
/	241 DKEILAYAKAGVAEEVLLAIRTVIAGGOKKELRYNKOLEAERGIKKAITANISIG	300	
/	301 AAPLLIAYASYALFWYGTTLVLSEGYISIGCVLTYFESTVJGAPSQGQSPSIEAFANARG	360	
/	301 AAPLLIAYASYALFWYGTTLVLSEGYISIGCVLTYFESTVJGAPSQGQSPSIEAFANARG	360	
361	AAYEIKIDNPKNSIDSYSKSGKPKDN1KGNLEPRNTVPSKKEVILKGJNLKVGQSG	420	
361	AAYEIKIDNPKNSIDSYSKSGKPKDN1KGNLEPRNTVPSKKEVILKGJNLKVGQSG	420	
421	QTVVALVGNISGCKSSTSIVQLMQLYDPTGMVSYDQDRTINTFLRBTIGVYSQEPYL	480	
421	QTVVALVGNISGCKSSTSIVQLMQLYDPTGMVSYDQDRTINTFLRBTIGVYSQEPYL	480	
481	ATTAAENIRYGRNVNTDEIEKAVKEANAYDFTMKLPHKFDTLVGERGAQSGCOKORIA	540	

Db	481	ATTAAENTRYGRENVTMDEIEKAKVKEANAYDFPMKLPHKFDLTVGERGAOLSGGQKORIA	540
Qy	541	IARALVRNPKILLIDEATSALDTESEAVVQVALDKARKGRRTTIVIAHRLSTVNADYTAG	600
Db	541	IARALVRNPKILLIDEATSALDTESEAVVQVALDKARKGRRTTIVIAHRLSTVNADYTAG	600
Qy	541	IARALVRNPKILLIDEATSALDTESEAVVQVALDKARKGRRTTIVIAHRLSTVNADYTAG	600
Db	601	FDDGIVVERGNHIDELMKKGIGYFKLYTMOTAGNEVELNAADESSEBDALEMSNDRS	660
Qy	601	FDDGIVVERGNHIDELMKKGIGYFKLYTMOTAGNEVELNAADESSEBDALEMSNDRS	660
Db	661	SIRKRSTRSRSTRSGSQQRDLKSTREALDESIPPSFWRIMKLNTTEMWPFVVGFCALL	720
Qy	661	SIRKRSTRSRSTRSGSQQRDLKSTREALDESIPPSFWRIMKLNTTEMWPFVVGFCALL	720
Ddb	721	NGLQPAFAIFSKILGVFRIDDPPTKRONSNLFSSLFLALGISSFITFFLOGFTFGKA	780
Qy	721	NGLQPAFAIFSKILGVFRIDDPPTKRONSNLFSSLFLALGISSFITFFLOGFTFGKA	780
Db	781	GEILITGRLLRMVFREMLRQWDSPWDPKNTTGALTTRLANDAQVKGAIGSRLAVITONI	840
Qy	781	GEILITGRLLRMVFREMLRQWDSPWDPKNTTGALTTRLANDAQVKGAIGSRLAVITONI	840
Db	841	ANLGCGIIISPIFYGHQLTILLATVPIATAIGVEMKULSGQALKDCKKELEGAKIAEA	900
Qy	841	ANLGCGIIISPIFYGHQLTILLATVPIATAIGVEMKULSGQALKDCKKELEGAKIAEA	900
Ddb	901	IENPFTVVSITQEOPFERNYAQSLQPVTRNSLRKAHIFGITTSFTQAMMMFSYAGCFREG	960
Qy	901	IENPFTVVSITQEOPFERNYAQSLQPVTRNSLRKAHIFGITTSFTQAMMMFSYAGCFREG	960
b	961	AYLVHQKMSFEDYLIVPSAVVGAIVAGQVSSFAPDYYAKAKISAAHHIMILEKTPLIDS	1020
b	961	AYLVHQKMSFEDYLIVPSAVVGAIVAGQVSSFAPDYYAKAKISAAHHIMILEKTPLIDS	1020
y	1021	YSTEGLMPNTLEGNNTPEGVWNYPTPRDPIYLOGISLEVKKGQTIALVSSGGCRSTVV	1080
b	1021	YSTEGLMPNTLEGNNTPEGVWNYPTPRDPIYLOGISLEVKKGQTIALVSSGGCRSTVV	1080
y	1081	QLERFYDPLACKVLLIGKIKRNQWLRHLGIVTSQEPILFDCSIARENIAYGDNRSVV	1140
b	1081	QLERFYDPLACKVLLIGKIKRNQWLRHLGIVTSQEPILFDCSIARENIAYGDNRSVV	1140
y	1141	SOBETRAAKEANIHAFTIESIPNPKYSTKVEDKGFTGOLSGGOKORIAALARVLQPHILLID	1200
b	1141	SOBETRAAKEANIHAFTIESIPNPKYSTKVEDKGFTGOLSGGOKORIAALARVLQPHILLID	1200
y	1201	EATSAALDTESKEVVOBALDKAREGTCITVIAHRLSTIQNADLIVVPGNRVKGHTHQQL	1260
b	1201	EATSAALDTESKEVVOBALDKAREGTCITVIAHRLSTIQNADLIVVPGNRVKGHTHQQL	1260
y	1261	LAQKGJYFMSMVQAGTKRQ	1280
b	1261	LAQKGJYFMSMVQAGTKRQ	1280
SUIT 5			
Sequence 3, Application US/09817762			
Patent No. 6858724			
GENERAL INFORMATION:			
APPLICANT: Spalding, Edgar P.			
APPLICANT: No. 6858774, Bosl.			
TITLE OF INVENTION: MDR-Like ABC Transporter Gene From			
TITLE OF INVENTION: Plants			
FILE REFERENCE: 133238-00061			
CURRENT APPLICATION NUMBER: US/09/817 762			
CURRENT FILING DATE: 2001-03-26			
PRIOR APPLICATION NUMBER: PCT/US99/22263			
PRIOR FILING DATE: 1999-09-24			
PRIOR APPLICATION NUMBER: US 60/101, 814			
PRIOR FILING DATE: 1998-09-25			
NUMBER OF SEQ ID NOS: 14			
SOFTWARE: FastSEQ for Windows Version 4.0			

SEQ ID NO 3
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 LOCATION INFORMATION:
 DATABASE ACCESSION NUMBER: Genbank P018183
 DATABASE ENTRY DATE: 1997-11-01
 US-09-817-762-3

Query Match 100 %; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1280; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MDLEGDRNGGACKKCPNPKCLNNKSEKDCKEKKCPTRVSFSMPRSNWLDKLYMVGTLLAII 60
 Db 1 MDLEGDRNGGACKKCPNPKCLNNKSEKDCKEKKCPTRVSFSMPRSNWLDKLYMVGTLLAII 60
 Qy 61 HGAAGLPLMLVQEMTDIFANAGNLIEDMSNITNRSDINDTGFEMMLEDMDTRAYYYSG 120
 Db 61 HGAAGLPLMLVQEMTDIFANAGNLIEDMSNITNRSDINDTGFEMMLEDMDTRAYYYSG 120
 Qy 121 IGAGVLYAYIQVSFWCLIAAGROTHKIRKOFFHAIRKOBIGFVDHGELNTRIDDS 180
 Db 121 IGAGVLYAYIQVSFWCLIAAGROTHKIRKOFFHAIRKOBIGFVDHGELNTRIDDS 180
 Qy 181 KINEVICKIGMFQSMATTFEGPFIYCFTRGKLTLYLAISPVGLSAAWAKLISFT 240
 Db 181 KINEVICKIGMFQSMATTFEGPFIYCFTRGKLTLYLAISPVGLSAAWAKLISFT 240
 Qy 241 DKELLAYAKAGAYAEVLAIAITVIAGQKCELERTNKNLBEAKRIGKKAITANISIG 300
 Db 241 DKELLAYAKAGAYAEVLAIAITVIAGQKCELERTNKNLBEAKRIGKKAITANISIG 300
 Qy 301 AAFLLTIAYSLAFWYGTTLVLSGEYSQGVLTIVFFSTLIGFSGVGASPSTEAFNARG 360
 Db 301 AAFLLTIAYSLAFWYGTTLVLSGEYSQGVLTIVFFSTLIGFSGVGASPSTEAFNARG 360
 Qy 361 AAYBIFKIDNKPSPIDSYSKSGKHPDNTKGNLEFRATHFSYSPSRKEYTKILKGNLKVQSG 420
 Db 361 AAYBIFKIDNKPSPIDSYSKSGKHPDNTKGNLEFRATHFSYSPSRKEYTKILKGNLKVQSG 420
 Qy 421 QTVVALVENISGCCKSSTTIVOLMQLRYDPTGMVSYDQDRTINVRFLREIIGVVSQEPVLF 480
 Db 421 QTVVALVENISGCCKSSTTIVOLMQLRYDPTGMVSYDQDRTINVRFLREIIGVVSQEPVLF 480
 Qy 481 ATTIAENTRYGENVTIDEIKAVKANEANDTMLKPHKDPLVGERAOISGGOKORIA 540
 Db 481 ATTIAENTRYGENVTIDEIKAVKANEAYDFIMCLPHKDPLVGERAOISGGOKORIA 540
 Qy 541 IARALVNPKILLDEATSLDTSEAVTQVALDKARKGRITIVIAHRLSTVNADYAG 600
 Db 541 IARALVNPKILLDEATSLDTSEAVTQVALDKARKGRITIVIAHRLSTVNADYAG 600
 Qy 601 FDDGTYVEKGNDHBLMKRGKTYKLVMTQAGNBVELENNAADESKSEDALEMSSNDRS 660
 Db 601 FDDGTYVEKGNDHBLMKRGKTYKLVMTQAGNBVELENNAADESKSEDALEMSSNDRS 660
 Qy 661 SJRKCSRSTRSRSQADRKLTSEKADESKSEDALEMSSNDRS 720
 Db 661 SJRKCSRSTRSRSQADRKLTSEKADESKSEDALEMSSNDRS 720
 Qy 721 NGGLQPAFAIIFSKLIGFTRDDPETRQNSNLFSLFLLAGIISFTFLOGFTGKA 780
 Db 721 NGGLQPAFAIIFSKLIGFTRDDPETRQNSNLFSLFLLAGIISFTFLOGFTGKA 780
 Qy 781 GEILTKRILRYMFRSMLEQDVSNFDDPQNTTGALTTRLANDAQVKGAIAGSRLAVTONI 840
 Db 781 GEILTKRILRYMFRSMLEQDVSNFDDPQNTTGALTTRLANDAQVKGAIAGSRLAVTONI 840
 Qy 841 ANGTGTLIISFYGMWLTLLIAAVPIATAIAGYVEMKNSQALIKDCKBLEGRGKATEA 900
 Db 841 ANGTGTLIISFYGMWLTLLIAAVPIATAIAGYVEMKNSQALIKDCKBLEGRGKATEA 900

Qy 901 IENFRITVSVLTOBQPERMYAQSLQVPRNSLRKAIIGGITFSFTQAMMIFSYACGCRFG 960
 Db 901 IENFRITVSVLTOBQPERMYAQSLQVPRNSLRKAIIGGITFSFTQAMMIFSYACGCRFG 960
 Qy 961 AYLVAHKLMSPEDDVLLFSAVFGAMAVGOVSSFPADYAKAKISAHITMIIEKTPLIDS 1040
 Db 961 AYLVAHKLMSPEDDVLLFSAVFGAMAVGOVSSFPADYAKAKISAHITMIIEKTPLIDS 1040
 Qy 1021 YSTEGLMPNTELEGNTTFRGEVYPRAYTPRDPDPLVLOCISLEVKGOTLALYGSGCCSKSTVV 1080
 Db 1021 YSTEGLMPNTELEGNTTFRGEVYPRAYTPRDPDPLVLOCISLEVKGOTLALYGSGCCSKSTVV 1080
 Qy 1081 QLEREYDPLAKVLDGEKIRKVNQMRHLIGVSQEPILFDOSIAETAYGDSNSRVV 1140
 Db 1081 QLEREYDPLAKVLDGEKIRKVNQMRHLIGVSQEPILFDOSIAETAYGDSNSRVV 1140
 Qy 1141 SQEEITRAKEANIAHAFIESLPNKYSTKVGDKGQOKQRATIARALVROPHILLD 1200
 Db 1141 SQEEITRAKEANIAHAFIESLPNKYSTKVGDKGQOKQRATIARALVROPHILLD 1200
 Qy 1201 EATSLADTESKVKVOEALDKAREGTCIVIAHRLSTIONADLIVVFQNGRKVEHGHQQL 1260
 Db 1201 EATSLADTESKVKVOEALDKAREGTCIVIAHRLSTIONADLIVVFQNGRKVEHGHQQL 1260
 Qy 1261 LAQKGTYFMSVSYQAGTKRQ 1280
 Db 1261 LAQKGTYFMSVSYQAGTKRQ 1280

RESULT 6
 US-09-584-586-4
 Sequence 4, Application US/09584586
 Patent No. 6733150

GENERAL INFORMATION:
 / APPLICANT: Sorrentino, Brian
 / INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 / TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 / FILE REFERENCE: 1340-1-021CIP
 / CURRENT APPLICATION NUMBER: US/09/584,586
 / CURRENT FILING DATE: 2000-05-31
 / EARLIER APPLICATION NUMBER: US 60/066,988
 / EARLIER FILING DATE: 1998-05-28
 / EARLIER APPLICATION NUMBER: PCT/US99/11825
 / EARLIER FILING DATE: 1999-05-27
 / NUMBER OF SEQ ID NOS: 16
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 4
 / LENGTH: 1280
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE: OTHER INFORMATION: Human MDR 185-V
 / OTHER INFORMATION: Human MDR 185-V
 US-09-584-586-4

Query Match 100 %; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGGAKKCPNPKCLNNKSEKDCKEKKCPTRVSFSMPRSNWLDKLYMVGTLLAII 60
 Db 1 MDLEGDRNGGAKKCPNPKCLNNKSEKDCKEKKCPTRVSFSMPRSNWLDKLYMVGTLLAII 60
 Qy 61 HGAGLPLMLVQEMTDIFANAGNLIEDMSNITNRSDINDTGFEMMLEDMDTRAYYYSG 120
 Db 61 HGAGLPLMLVQEMTDIFANAGNLIEDMSNITNRSDINDTGFEMMLEDMDTRAYYYSG 120
 Qy 121 IGAGLVVAYIOVSFWCLIAAGROTHKIRKOFFHAIRKOBIGFVDHGELNTRIDDS 180
 Db 121 IGAGLVVAYIOVSFWCLIAAGROTHKIRKOFFHAIRKOBIGFVDHGELNTRIDDS 180
 Qy 181 KINEVICKIGMFQSMATTFEGPFIYCFTRGKLTLYLAISPVGLSAAWAKLISFT 240

Db	181 KINEVIGDKIGMFQSMATPPTGFIYGPTRGMKLTIVLIAISPVGLSAAWAKILSSPT	240	RESULT 7
Qy	241 DKELLAYAKIGAVAEVLAAIRTVAFGGOKKELLYNKLEAKRIGKKATTANISG	300	US-08-583-276-19
Db	241 DKELLAYAKIGAVAEVLAAIRTVAFGGOKKELLYNKLEAKRIGKKATTANISG	300	; Sequence 19, Application US/08583276
Qy	301 AAFLLIYASALAFAYGTTLVSLGEYSIGCAGYLTVFFSVLGAFAQSPSIEAFANARG	360	; Patent No. 5831536
Db	301 AAFLLIYASALAFAYGTTLVSLGEYSIGCAGYLTVFFSVLGAFAQSPSIEAFANARG	360	; GENERAL INFORMATION:
Qy	301 AAFLLIYASALAFAYGTTLVSLGEYSIGCAGYLTVFFSVLGAFAQSPSIEAFANARG	360	; APPLICANT: McDonagh, Kevin T.
Db	301 AAFLLIYASALAFAYGTTLVSLGEYSIGCAGYLTVFFSVLGAFAQSPSIEAFANARG	360	; APPLICANT: Niemuth, Arthur
Qy	361 AAYEIPKIDKPKSDSYSKSGHKPDNIGKLENPEFRNVHFSYPSRSKEYKVLKGMLNKVQSG	420	; APPLICANT: Tolbroshev, Paul
Db	361 AAYEIPKIDKPKSDSYSKSGHKPDNIGKLENPEFRNVHFSYPSRSKEYKVLKGMLNKVQSG	420	; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
Qy	421 QVALVGNSGGKSTTQLMQLRDPDTEGVSVQDQDIRINTVFLREIGVSIQSPKF	480	; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
Db	421 QVALVGNSGGKSTTQLMQLRDPDTEGVSVQDQDIRINTVFLREIGVSIQSPKF	480	; NUMBER OF SEQUENCES: 19
Qy	421 ATTAEINRIGRENTMDIEKAVEREANAYDFIMKLPHFDTLVYGERGAQLSGQKQRA	540	; CORRESPONDENCE ADDRESS:
Db	421 ATTAEINRIGRENTMDIEKAVEREANAYDFIMKLPHFDTLVYGERGAQLSGQKQRA	540	; ADDRESSEE: Carella, Byrne, Bain, Giltellan,
Qy	541 TARALVRNPKILLDEATSALDTESEAVYQVALDKARKSRTTIVLAHRISTVNADVAIG	600	; STREET: Cecchi & Stewart
Db	541 TARALVRNPKILLDEATSALDTESEAVYQVALDKARKSRTTIVLAHRISTVNADVAIG	600	; STREET: 6 Becker Farm Road
Qy	601 FDDGTIVVKGNHDLMKEGIYFLVUTMAGNEVELENADESKETDALEMSNDRS	660	; CITY: Roseland
Db	601 FDDGTIVVKGNHDLMKEGIYFLVUTMAGNEVELENADESKETDALEMSNDRS	660	; STATE: New Jersey
Qy	661 SLIRRSTRRSVRSGAQDRKLSTKEALDSIPPVSFWIMKUNLNEWYFVVGVFCAII	720	; COUNTRY: USA
Db	661 SLIRRSTRRSVRSGAQDRKLSTKEALDSIPPVSFWIMKUNLNEWYFVVGVFCAII	720	; ZIP: 07068
Qy	7221 NGGLOPAFALIFSKLIGVTRIDDETKRONSFLSLPLALGISFTFLQOFTFGKA	780	; COMPUTER READABLE FORM:
Db	7221 NGGLOPAFALIFSKLIGVTRIDDETKRONSFLSLPLALGISFTFLQOFTFGKA	780	; COMPUTER TYPE: 3.5 inch diskette
Qy	7221 ANLFGGIISIPIYGKQIQLTLLAIPVIIAGYVEMKNSGQALKDKKELEGKIAATE	900	; COMPUTER: IBM PS/2
Db	7221 ANLFGGIISIPIYGKQIQLTLLAIPVIIAGYVEMKNSGQALKDKKELEGKIAATE	900	; OPERATING SYSTEM: PC-DOS
Qy	781 GEILTKRJYMFPSMLRDQSWPFDPKTTGALTTRLANDAAQYKGAIQSLRAVITONI	840	; SOFTWARE: DW4_V2
Db	781 GEILTKRJYMFPSMLRDQSWPFDPKTTGALTTRLANDAAQYKGAIQSLRAVITONI	840	; CURRENT APPLICATION DATA:
Qy	841 ANLFGGIISIPIYGKQIQLTLLAIPVIIAGYVEMKNSGQALKDKKELEGKIAATE	900	; APPLICATION NUMBER: US/08/583,276
Db	841 ANLFGGIISIPIYGKQIQLTLLAIPVIIAGYVEMKNSGQALKDKKELEGKIAATE	900	; FILING DATE: 05-JAN-1996
Qy	901 IENFRTVVSLTOEQRPERMYAOSLQYPTNSLRKAHIFGIFTSTQAMNYFSTAGCPFG	960	; CLASSIFICATION: 435
Db	901 IENFRTVVSLTOEQRPERMYAOSLQYPTNSLRKAHIFGIFTSTQAMNYFSTAGCPFG	960	; PRIOR APPLICATION DATA:
Qy	961 AYLAHKLMSFEDVLLVPSAVVFGAMAVQSYSSPADYAKISAHHIMIETKPLIDS	1020	; APPLICATION NUMBER: 08/332,444
Db	961 AYLAHKLMSFEDVLLVPSAVVFGAMAVQSYSSPADYAKISAHHIMIETKPLIDS	1020	; FILING DATE: 31-OCT-1994
Qy	1021 YSTEGLMPMTLEGNTFGEVENYPTRPDIPLVQGLSLFVKGKOTLAVGSSCGKSTVY	1080	; APPLICATION NUMBER: 07/887,712
Db	1021 YSTEGLMPMTLEGNTFGEVENYPTRPDIPLVQGLSLFVKGKOTLAVGSSCGKSTVY	1080	; FILING DATE: 22-MAY-1992
Qy	1141 SQEIVRAKEANITHAFISLPLNPKYSTKVGDKTOLSGQKQRIATAALVROPHILLLD	1200	; INFORMATION FOR SEQ ID NO: 19:
Db	1141 SQEIVRAKEANITHAFISLPLNPKYSTKVGDKTOLSGQKQRIATAALVROPHILLLD	1200	; LENGTH: 1280 amino acids
Qy	1081 QLLERFYDLAGKVLDGGEIKRNLVQMLAHGIVSOPPLFDCSIANIAYGDNRSVY	1140	; TYPE: amino acid
Db	1081 QLLERFYDLAGKVLDGGEIKRNLVQMLAHGIVSOPPLFDCSIANIAYGDNRSVY	1140	; STRANDEDNESS:
Qy	1201 EATSLDTSKEVYQEALIKAREGRTCTVIAHRLUSTIONADLIVFONGRVKEGHGTHQ	1260	; TOPOLOGY: linear
Db	1201 EATSLDTSKEVYQEALIKAREGRTCTVIAHRLUSTIONADLIVFONGRVKEGHGTHQ	1260	; MOLECULE TYPE: protein
Qy	1261 LAQKGIYFPMVSYQAGTKRQ	1280	; DESCRIPTION: protein
Db	1261 LAQKGIYFPMVSYQAGTKRQ	1280	; US-08-583-276-19
Qy	301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG	360	Query Match 99.9%; Score 6428; DB 1; Length 1260;
Db	301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG	360	Best Local Similarity 99.9%; Pred. No. 0; Indels 0; Gaps 0; Matches 1279; Conservative 1; Mismatches 0;
Qy	121 1GAGVLVAYIQLQSFNCIAAGROIHKIRKOFHAIMROEIGMFDYHVGELNTRLDDVS	180	Oy 1 MDLEGDRNGGAKKNPKLNNSKEDCKKEKPTVFSMPRYSNWIDKLVMVGTLLAII 60
Db	121 1GAGVLVAYIQLQSFNCIAAGROIHKIRKOFHAIMROEIGMFDYHVGELNTRLDDVS	180	Db 1 MDLEGDRNGGAKKNPKLNNSKEDCKKEKPTVFSMPRYSNWIDKLVMVGTLLAII 60
Qy	61 HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFMNLDEDMTRYAYYYSG	120	Oy 61 HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFMNLDEDMTRYAYYYSG 120
Db	61 HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFMNLDEDMTRYAYYYSG	120	Db 61 HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSDINDTGFMNLDEDMTRYAYYYSG 120
Qy	181 KINEVIGDKIGMFQSMATFPFGPIQFTGKMLTIVLISPVGLSAAWAKILSSFT	240	Oy 181 KINEVIGDKIGMFQSMATFPFGPIQFTGKMLTIVLISPVGLSAAWAKILSSFT 240
Db	181 KINEVIGDKIGMFQSMATFPFGPIQFTGKMLTIVLISPVGLSAAWAKILSSFT	240	Db 181 KINEVIGDKIGMFQSMATFPFGPIQFTGKMLTIVLISPVGLSAAWAKILSSFT 240
Qy	241 DKELLAYAKAGAVAEVLAAARTVIFGQKKELEYINKOLEAKRIGKKAITANISG	300	Oy 241 DKELLAYAKAGAVAEVLAAARTVIFGQKKELEYINKOLEAKRIGKKAITANISG 300
Db	241 DKELLAYAKAGAVAEVLAAARTVIFGQKKELEYINKOLEAKRIGKKAITANISG	300	Db 241 DKELLAYAKAGAVAEVLAAARTVIFGQKKELEYINKOLEAKRIGKKAITANISG 300
Qy	301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG	360	Qy 301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG 360
Db	301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG	360	Db 301 AAFLLIYASYALAFWYGTTLVLSGEYSIGQYLTVFVFSVLIGAFSVOQASPIEAPANARG 360

Qy	1	M DLEGDRNGGAEBKKNNFKLNNKSKDKKERPTVSFSMFRYSNWLDKLNVYGLAII	60		1078	TVVQOLLERFDPLAKVLLDJKKEIKOLNQWMLRAHGLVSQEPILFDCSENAYGDN	1137
Db	1	M DLEGDRNGGAEBKKNNFKLNNKSKDKKERPTVSFSMFRYSNWLDKLNVYGLAII	60	Db	1141	RVVSQEPIWRAKENANHARIESIINKYSTRVGDKTQLSGGOKRIATARAIVQPHL	1200
Qy	61	HGAGLPLMLVFGDMTDTFANAGNLCDLGALLFNNTNSNITDTVPVMNLEDMDTRYAY	120	Qy	1138	RVVSQEPIWRAKENANHARIESIINKYSTRVGDKTQLSGGOKRIATARAIVQPHL	1197
Db	61	HGAGLPLMLVFGDMTDTFANAGNLCDLGALL--TNSNITDTVPVMNLEDMDTRYAY	117	Db	1201	LDEDEALDTSEKEVQVQALDKAREGRCTIVIAHRLSTQNADJLWVQNGRYVEHGTH	1260
Qy	1221	YSGIGAGVLYVAYIOVSFWCLAAAGROTHKIRKOPFHAIMROBIGNEDVHDGEINTRLTD	180	Qy	1198	LDEDEALDTSEKEVQVQALDKAREGRCTIVIAHRLSTQNADJLWVQNGRYVEHGTH	1257
Db	118	YSGIGAGVLYVAYIOVSFWCLAAAGROTHKIRKOPFHAIMROBIGNEDVHDGEINTRLTD	177	Db	1261	QOLLAQKGIYSMSVQAGKRO	1283
Qy	181	DVKSKNEGICDKIGMPQSMATPFTGRWKLTVLAISPVLGLSAAVAKILS	240	Qy	1258	QOLLAQKGIYSMSVQAGKRO	1280
Db	178	DVKSKNEGICDKIGMPQSMATPFTGRWKLTVLAISPVLGLSAAVAKILS	237	Db	1261	QOLLAQKGIYSMSVQAGKRO	1283
Qy	241	SFTDELLAYAKAGVAEVLAAIRVIAFGQKELERINKNLEAKRIGKKAITANI	300	RESULT 6	US-09-584-586-2		
Db	238	SFTDELLAYAKAGVAEVLAAIRVIAFGQKELERINKNLEAKRIGKKAITANI	297		Sequence 2, Application US/09584586		
Qy	301	SIGAAFLLIYAYSLAFLFWYGTTLVLSKEYSIGQVLTIVFSYLIGAFSVQAPSIEAFN	360		Patent No. 6933150		
Db	298	SIGAAFLLIYAYSLAFLFWYGTTLVLSKEYSIGQVLTIVFSYLIGAFSVQAPSIEAFN	357		GENERAL INFORMATION:		
Qy	361	ARGAAFEIPIKLNKPSIDSYSKSGKHPDNKGNLDFRNTYHESYPSRKEVYKLGUNLK	420		APPLICANT: Sorrentino, Brian		
Db	358	ARGAAFEIPIKLNKPSIDSYSKSGKHPDNKGNLDFRNTYHESYPSRKEVYKLGUNLK	417		APPLICANT: Bunting, Kevin		
Qy	421	QSGQTVALVGNSGCKSTTOLMQLRYDPTGMSVSDQDQIRTINVRFELIIGVVSQEP	480		TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH		
Db	418	QSGQTVALVGNSGCKSTTOLMQLRYDPTGMSVSDQDQIRTINVRFELIIGVVSQEP	477		FILE REFERENCE: 1340-1-021LIP		
Qy	481	VLFATTIANENTRYGREDVTMDBIEKAVKEANAYDFIMKLKPDKFDTLVGERAOLSIGGOKQ	540		CURRENT FILING DATE: 2000-05-31		
Db	478	VLFATTIANENTRYGREDVTMDBIEKAVKEANAYDFIMKLKPDKFDTLVGERAOLSIGGOKQ	537		CURRENT APPLICATION NUMBER: US 60/086,988		
Qy	541	RIATARALVRNPKILLDEATSALDTSEAVYQVALDKARKGRITIVIAHRLSTVNADV	600		EARLIER FILING DATE: 1998-05-28		
Db	538	RIATARALVRNPKILLDEATSALDTSEAVYQVALDKARKGRITIVIAHRLSTVNADV	597		EARLIER APPLICATION NUMBER: PCT/US99/11825		
Qy	601	IAGFDGGV1VERGNHDBLMKRGIGYPLVMTOTAGNEELENAADESKEDDTLEMSSHD	660		EARLIER FILING DATE: 1999-05-27		
Db	598	IAGFDGGV1VERGNHDBLMKRGIGYPLVMTOTAGNEELENAADESKEDDTLEMSSHD	657		NUMBER OF SEQ ID NOS: 16		
Qy	661	SGSSLJRKSTRRSYRGSGODRKLSKTEALDESIPPVSFRWIMCLNLTEMVYFTVGVFC	720		SOFTWARE: Patentin Ver. 2.0		
Db	658	SGSSLJRKSTRRSYRGSGODRKLSKTEALDESIPPVSFRWIMCLNLTEMVYFTVGVFC	717		SEQ ID NO 2		
Qy	721	AINGGLQPAFVISSKIGIGFTRNDAETKRNSNLPSLFLVLGIVSPITPELOGFTF	780		LENGTH: 1280		
Db	718	AINGGLQPAFVISSKIGIGFTRNDAETKRNSNLPSLFLVLGIVSPITPELOGFTF	777		TYPE: PRT		
Qy	781	GRAGEILTRURYVFRSMQRDVSMEFDPKNTTGALTTRILANDAQVKAIGSPLAIT	840		ORGANISM: Homo sapiens		
Db	778	GRAGEILTRURYVFRSMQRDVSMEFDPKNTTGALTTRILANDAQVKAIGSPLAIT	837		FEATURE:		
Qy	841	ONIANGTGIIISLIGWOLTLLIAIPIA1AGVEMKMSGOALKKELEGAKTA	900		OTHER INFORMATION: Human MDR 185-G		
Db	838	ONIANGTGIIISLIGWOLTLLIAIPIA1AGVEMKMSGOALKKELEGAKTA	897		US-09-584-586-2		
Qy	901	TEA1ENPRTVSLTOBOKPERMYDQS1LQPVYRNSLRKAHLFGITTSPTQAMMFYSYACCF	960		Query Match		
Db	898	TEA1ENPRTVSLTOBOKPERMYDQS1LQPVYRNSLRKAHLFGITTSPTQAMMFYSYACCF	957		Best Local Similarity		
Qy	961	RFGAYLVAHSLMSFEDVLLVSAVVGAMAVGVSSFAPDVAKAVSAHLLIMITPL	1020		Matches 1238;		
Db	958	RFGAYLVAHSLMSFEDVLLVSAVVGAMAVGVSSFAPDVAKAVSAHLLIMITPL	1017		Score 6212.5;		
Qy	1021	IDSYSTEGLKPNTLEGNTFNEWVNYPTRLDIPVQGLSLEVKGQTALVGSSCGKS	1080		DB 2;		
Db	1018	IDSYSTEGLKPNTLEGNTFNEWVNYPTRLDIPVQGLSLEVKGQTALVGSSCGKS	1077		Length 1280;		
Qy	1081	TVVQOLLERFDPLAKVLLDJKKEIKOLNQWMLRAHGLVSQEPILFDCS1SENAYGDN	1140		Length 1280;		

FILE REFERENCE: 015260-402100US
; CURRENT APPLICATION NUMBER: US 09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIORITY NUMBER: US 60/177,410
; PRIORITY FILING DATE: 2000-01-20
; NUMBER OF SEQ ID: NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match Score 6203.5%; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; N mismatches 25; Indels 3; Gaps 1;

Qy 1 MDLEGDRNGGAEKONFKLANKSKDKKKRPTVFSMFRYSWNLKLYMVGLAAII 60
Db 1 MDLEGDRNGGAKONFKLANKSKDKKKRPTVFSMFRYSWNLKLYMVGLAAII 60
Qy 61 HGAGLPLMLMVGDMTDTFANAGNIGDGLALLFNTNTNSNITDTFVPMVNLBEDMTRAYY 120
Db 61 HGAGLPLMLMVGDMTDTFANAGNIGDGLALLFNTNTNSNITDTFVPMVNLBEDMTRAYY 117
Qy 721 AINGGQPAFVIFSKLIGIPIRNDAAETKRONSNLFLFIVLGIIVSFTEFLOGTF 780
Db 718 AINGGQPAFVIFSKLIGIPIRNDAAETKRONSNLFLFIVLGIIVSFTEFLOGTF 777
Qy 781 GKAEGILTKRLRYMVFPSMLRDQVSWDDPKNTGALTTRLANDAQVKGAGSRLAII 840
Db 778 GKAEGILTKRLRYMVFPSMLRDQVSWDDPKNTGALTTRLANDAQVKGAGSRLAII 837
Qy 841 QNTANLGTLGIIISLIGQMLTLLLAIVPIIAIAGVYEMKMSGOALIKDKELEGACKIA 900
Db 838 QNTANLGTLGIIISLIGQMLTLLLAIVPIIAIAGVYEMKMSGOALIKDKELEGACKIA 897
Qy 901 TEAIENPRTVVSITOQEKFERNYDQSLOPVYNLSLRKAIIHISITESTPSTQAMMFSTAGCF 960
Db 898 TEAIENPRTVVSITOQEKFERNYDQSLOPVYNLSLRKAIIHISITESTPSTQAMMFSTAGCF 957
Qy 961 RFGAYLVASHSMSFEDVLLVSAVFGAMAAGVYSSAPDAKAKSAAHIMIETPL 1020
Db 958 RFGAYLVASHSMSFEDVLLVSAVFGAMAAGVYSSAPDAKAKSAAHIMIETPL 1017
Qy 1021 IDSYSTEGLKPNTLEGNVTFNEVNFYPTRLDIPVQLQSLVEYKRGOTLALVGSGGCKS 1080
Db 1018 IDSYSTEGLMPNTLEGNVTFGEVVFNTPTRPDIPVQLQSLVEYKRGOTLALVGSGGCKS 1077
Qy 1081 TVVOLLERFYDPLAKVVLIDGKEIKOLNYQMLRAHLGLIVSQEPILFDCISIENAYCDNS 1140
Db 1078 TVVOLLERFYDPLAKVVLIDGKEIKOLNYQMLRAHLGLIVSQEPILFDCISIENAYCDNS 1137
Qy 1141 RYVSQEEITRAKEANIHAFIESLPNKYSTRVDKGTOISGGOKQRIARALVRQPHL 1200
Db 1138 RYVSQEEITRAKEANIHAFIESLPNKYSTRVDKGTOISGGOKQRIARALVRQPHL 1197
Qy 1201 LDEATSADTESEKVVOEALDKAREGRCTCIVIAHRSLISTQNDLIVFQNGRKETHH 1260
Db 1198 LDEATSADTESEKVVOEALDKAREGRCTCIVIAHRSLISTQNDLIVFQNGRKETHH 1257
Qy 1261 QOLIAQKGYFMSMVSQGAKRO 1283
Db 1258 QOLIAQKGYFMSMVSQACTKRQ 1280
Qy 1318 QOLIAQKGYFMSMVSQACTKRQ 1281
Db 1317 QOLIAQKGYFMSMVSQACTKRQ 1280
Qy 1367 QOLIAQKGYFMSMVSQACTKRQ 1281
Db 1366 QOLIAQKGYFMSMVSQACTKRQ 1280
Qy 1418 QSGQTVALGVNSGCGKSTTVOLMORLYDPTEGMVSYGDQDIRTINRFREIIGVSQEP 480
Db 1398 QSGQTVALGVNSGCGKSTTVOLMORLYDPTEGMVSYGDQDIRTINRFREIIGVSQEP 477
Qy 1481 VLFATTAENTRYGRDVTMDIEKVKANEAYDFIMKLPOKFDTLVRGERAQQLSGGQKQ 540
Db 1478 VLFATTAENTRYGRDVTMDIEKVKANEAYDFIMKLPOKFDTLVRGERAQQLSGGQKQ 537
Qy 1541 RIAJARALVRPKILLDEATSALDSEAVVOVQUALDKRGRTIVIAHRSLTVRNADV 600
Db 1538 RIAJARALVRPKILLDEATSALDSEAVVOVQUALDKRGRTIVIAHRSLTVRNADV 597
Qy 1601 TAGFDGIVTVEKGNHDELMKRGKJYFKLVTMOTAGNIELENAADSKEEDTLENISHD 660
Db 1598 TAGFDGIVTVEKGNHDELMKRGKJYFKLVTMOTAGNIELENAADSKEEDTLENISHD 657
Qy 1661 SGSSLLRKSRSPRSVRSQSOGRKLSTKEALDESITPPSVRIMKLNTEMPPVYGVFC 720
Db 1658 SRSSLRKSRSPRSVRSQSOGRKLSTKEALDESITPPSVRIMKLNTEMPPVYGVFC 717
Qy 1721 AINGGQPAFVIFSKLIGIPIRNDAAETKRONSNLFLFIVLGIIVSFTEFLOGTF 780
Db 1718 AINGGQPAFVIFSKLIGIPIRNDAAETKRONSNLFLFIVLGIIVSFTEFLOGTF 777

RESULT 7
US-09-767-594-2
; Sequence 2, Application US/09/767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Robert, Susan
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; Department of Health and Human Services
; APPLICANT: Department of Health and Human Services by Acridine Derivatives
; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

Query Match	96.3%	Score 6203.5;	DB 2;	Length 1280;	
Best Local Similarity	96.4%;	Pred. No. 0;			
Matches 1237; Conservatve 18; Mismatches 25; Indels 3; Gaps 1;					
Qy	1	M DLEDRNGGA EKKP KLNNSK KDKKER KER KETV SFSM P RYS NWL DKL MM YGT LAA I	60	Db	1018 IDSY STEG IMLPT LEGNT FGEV VNFY PTPD I PVLG S LEVK QGT L ALVG S GG GKS 1077
Db	1	M DLEDRNGGA EKKP KLNNSK KDKKER KER KETV SFSM P RYS NWL DKL MM YGT LAA I	60	Qy	1018 IDSY STEG IMLPT LEGNT FGEV VNFY PTPD I PVLG S LEVK QGT L ALVG S GG GKS 1077
Qy	61	H GAGL P LMM LVFG DM TD P A N G NL G D L G A L L E N T I S N I T D T V P M N L E D M T R Y A Y	120	Db	1078 TVVQ L L E R Y D P L A G K V L D G K E T K L Q N V Q M L R H G I V S Q E P I L P D C S I S E N T A Y G D N S 1140
Db	61	H GAGL P LMM LVFG DM TD P A N G NL G D L G A L L E N T I S N I T D T V P M N L E D M T R Y A Y	120	Qy	1081 TVVQ L L E R Y D P L A G K V L D G K E T K L Q N V Q M L R H G I V S Q E P I L P D C S I S E N T A Y G D N S 1140
Qy	121	Y SGIG A G V L V A Y A Y I Q V S F W C L A A G R Q I H K I R K O F F H A I M R Q E G F W D Y H D V G E L N T L D	180	Db	1078 TVVQ L L E R Y D P L A G K V L D G K E T K L Q N V Q M L R H G I V S Q E P I L P D C S I S E N T A Y G D N S 1140
Db	118	Y SGIG A G V L V A Y A Y I Q V S F W C L A A G R Q I H K I R K O F F H A I M R Q E G F W D Y H D V G E L N T L D	177	Qy	1141 RV SQ E E V T R A E K A N H A F I E S L P N K S T R V D G K G T Q L S G G Q K O R I A L A R V C H G H T 1200
Qy	181	D Y SK I N E G I G D K I G M P Q S M A T T F T G F V G F T R G W K L T L V L I A I S P V G L S A A W A K I L S	240	Db	1138 RV SQ E E V T R A E K A N H A F I E S L P N K S T R V D G K G T Q L S G G Q K O R I A L A R V C H G H T 1197
Db	178	D Y SK I N E G I G D K I G M P Q S M A T T F T G F V G F T R G W K L T L V L I A I S P V G L S A A W A K I L S	237	Qy	1201 LD E D T A S D T E S E K V Y O F A L D K A R E G R T C I V A H R L S T I Q N A D J I V F O N G R V K E H G H T 1260
Qy	241	S P T D K E L L A Y A K A G A V E E V L A A I R T V I A R G Q K K E L E R Y N K N L E A R K R I G K K A T A N I	300	Db	1198 LD E D T A S D T E S E K V Y O F A L D K A R E G R T C I V A H R L S T I Q N A D J I V F O N G R V K E H G H T 1257
Db	238	S P T D K E L L A Y A K A G A V E E V L A A I R T V I A R G Q K K E L E R Y N K N L E A R K R I G K K A T A N I	297	Qy	1261 Q L L A Q K G I Y F P M S V Y Q A G K R Q 1283
Qy	301	S I G A A F L I Y A S Y A L A P W Y G T T L V L S K E Y S I G O V L T Y F F S V L I G A F S V Q A S P S I E A F N	360	Db	1258 Q L L A Q K G I Y F P M S V Y Q A G K R Q 1280
Db	298	S I G A A F L I Y A S Y A L A P W Y G T T L V L S K E Y S I G O V L T Y F F S V L I G A F S V Q A S P S I E A F N	357	Qy	RESULT 11 US-09-817-762-3 ; Sequence 3, Application US/09817762 ; Patent No. 685874 ; GENERAL INFORMATION: ; APPLICANT: Spalding, Edgar P. ; APPLICANT: No. 6858774, Bosl ; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From ; TITLE OF INVENTION: Plants ; TITLE OF INVENTION: Plant ; FILE REFERENCE: 132238-00061 ; CURRENT APPLICATION NUMBER: US/09/817,762 ; CURRENT FILING DATE: 2001-03-16 ; PRIOR APPLICATION NUMBER: PCT/US99/22363 ; PRIOR FILING DATE: 1999-09-24 ; PRIOR APPLICATION NUMBER: US 60/101,814 ; PRIOR FILING DATE: 1998-05-25 ; NUMBER OF SEQ ID NOS: 14 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO: 3 ; LENGTH: 1280
Qy	361	A R G A A F E P L K I I D N K P S I D S Y S K S G H K P D N T K G N L E F P R N V H F S Y P S R K V K L K G L N L K V	420	Db	US-09-817-762-3
Db	358	A R G A A Y I F K I I D N K P S I D S Y S K S G H K P D N T K G N L E F P R N V H F S Y P S R K V K L K G L N L K V	417	Qy	; PUBLICATION INFORMATION: ; PUBLICACION: Genbank P08183 ; DATABASE ACCESSION NUMBER: Genbank P08183 ; DATABASE ENTRY DATE: 1997-11-01
Qy	421	Q S G Q T V A L V G N S C G K S T T V Q M O R L Y D P T G E M V S D G Q D I P T V N V R F L E I G V V S Q E P	480	Db	Qy
Db	418	Q S G Q T V A L V G N S C G K S T T V Q M O R L Y D P T G E M V S D G Q D I P T V N V R F L E I G V V S Q E P	477	Db	Qy
Qy	481	V I F A T T I A E N I R Y G R E D V T M D E I K A V E K A N A Y D F I M K L P K Q E P D T L V G E R Q A L S G G Q K O	540	Db	Qy
Db	478	V I F A T T I A E N I R Y G R E N T V M D E I K A V E K A N A Y D F I M K L P K Q E P D T L V G E R Q A L S G G Q K O	537	Db	Qy
Qy	541	R I A R A L V R N P K I L L D E A T S A L D T E S A V V O Y A L D K A R G R T T I V A H R L S T V R N A D V	600	Db	Qy
Db	538	R I A R A L V R N P K I L L D E A T S A L D T E S A V V O Y A L D K A R G R T T I V A H R L S T V R N A D V	597	Db	Qy
Qy	601	I A G F D D G V I E V K G N H D E L M K E K G I Y F K L V T M O T A G N E I E L E N A D E S K S E I D T L E M S H D	660	Db	Qy
Db	598	I A G F D D G V I E V K G N H D E L M K E K G I Y F K L V T M O T A G N E V E L E N A D E S K S E I D A L E M S H D	657	Db	Qy
Qy	661	S C S S L I R K S T R S V R G S Q Q D R Q K L S T R E A L D E S I P P Y S F W R I M K L N T E W P Y F V G F C	720	Db	Qy
Db	658	S C S S L I R K S T R S V R G S Q Q D R Q K L S T R E A L D E S I P P Y S F W R I M K L N T E W P Y F V G F C	717	Db	Qy
Qy	721	A I N G G L O P A F A V I F S K L I G I F T R N D D A E T K R O N S N L F S L F L V G I V S F I T P F L Q G F T F	780	Db	Qy
Db	718	A I N G G L O P A F A V I F S K L I G I F T R N D D A E T K R O N S N L F S L F L V G I V S F I T P F L Q G F T F	777	Db	Qy
Qy	781	G K A G E I L T K R L R T M V F R S M L R Q D Y S W F D D P K N T G A L T R L A N D A A Q V G A G S R L A I T	840	Db	Qy
Db	778	G K A G E I L T K R L R T M V F R S M L R Q D Y S W F D D P K N T G A L T R L A N D A A Q V G A G S R L A I T	837	Db	Qy
Qy	841	Q N I A N L G T G I I I S I L Y G H O L T L L I A V P I L A I A G V E M K M S G A L D K K E L G A G K I A	900	Db	Qy
Db	838	Q N I A N L G T G I I I S I P Y G H O L T L L I A V P I L A I A G V E M K M S G A L D K K E L G A G K I A	897	Db	Qy
Qy	901	T E A I E N F R T V S L T Q O E K P E H M Y D S L O V E Y R N S L R K A I T F G I T S F T O M M Y F Y A G C P	960	Db	Qy
Db	898	T E A I E N F R T V S L T Q E Q K E H M Y A S L Q V F Y R N S L R K A H F G I T S F T Q M M Y S Y A G C P	957	Db	Qy
Qy	961	R F G A Y L V A H S L M S P E D V I L V S A U V F G A M V A G O V S S F A P P Y A K V S A A H I M I E K T P L	1020	Db	Qy
Qy	958	R F G A Y L V A H K L M S P E D V I L V S A U V F G A M V A G O V S S F A P P Y A K V S A A H I M I E K T P L	1017	Db	Qy
Qy	301	S I G A A F L I Y A S Y A L F W Y G T L V L S K E Y S I C Q V L T V F S L I G A F S V Q A S P S I E A F A N	360	Qy	1021 IDSY STEG IMLPT LEGNT FGEV VNFY PTPD I PVLG S LEVK QGT L ALVG S GG GKS 1080

298 SIGAAFLIYASYALAFWYGETTIVLSEGEYSIGQVLTFFSVLIGAFSYQASPSTEAPPN 357
 QY 361 ARGAAFEIYLIDNPKSISDYSKSKSHKDNLKGNIERPRVAFSYSPRKEVKILGLNLKV 420
 DB 358 ARGAYEIIPLKIDNPKSISDYSKSKSHKDNLKGNIERPRVAFSYSPRKEVKILGLNLKV 417
 QY 421 QSGQTVALVNGCGKSTTVQLMORLYDPTEGMVSVDGDIRTINVRFLREIIGVVSOP 480
 DB 418 QSGQTVALVNGCGKSTTVQLMORLYDPTEGMVSVDGDIRTINVRFLREIIGVVSOP 477
 QY 481 VLFPATTIANTRYGREDTMDEIEKAVKERANAYOPTIMKLPDKPFTLVGERGAOLSGGQKQ 540
 DB 478 VLFPATTIANTRYGRENTMDEIEKAVKERANAYOPTIMKLPHKFDTLVGERGAOLSGGQKQ 537
 QY 541 RIALARALTRNPKLILDEATSALDTESEAVVOYALDKARKGRITVIARHLSTVRNAVD 600
 DB 538 RIALARALTRNPKLILDEATSALDTESEAVVOYALDKARKGRITVIARHLSTVRNAVD 597
 QY 601 IAGPDDGVYVEKGNDHELMKKGYFKLVTMOTAGNEELENADEBESKEBDTLEMSHD 660
 DB 598 IAGPDDGVYVEKGNDHELMKKGYFKLVTMOTAGNEELENADEBESKEBDTLEMSHD 657
 QY 661 SGSSLIRKSTRRSYRGSCQDRKLSTKDALDESITPPVSFRWIMKLNLTTEMPFVVGYVC 720
 DB 658 SRSSLLRKSTRRSYRGSCQDRKLSTKDALDESITPPVSFRWIMKLNLTTEMPFVVGYTC 717
 QY 721 AINGGLQAFAVFSKIGIFTANDDAETKQRNSNLFSILFLVIGTSIFITFLQGT 780
 DB 718 AINGGLQAFAVFSKIGIFTANDDAETKQRNSNLFSILFLVIGTSIFITFLQGT 777
 QY 781 GKAEBILTRKLRYMFRSLRQDVSFWDFDKNTGALTIRLANDAQYKGAISSRLAAT 840
 DB 778 GKAEBILTRKLRYMFRSLRQDVSFWDFDKNTGALTIRLANDAQYKGAISSRLAAT 837
 QY 841 QNANLGCTTISLIGMOTLTLIAVPIATAGVVKMLSGOALDKKELEGAGKIA 900
 DB 838 QNANLGCTTISLIGMOTLTLIAVPIATAGVVKMLSGOALDKKELEGAGKIA 897
 QY 901 TEALENFTVUSTOEKREHYMDOSLQPYRNSLRKAHIFGTTSFQAMMYESIACP 960
 DB 898 TEALENFTVVLSTOEKEHEHYZQSLQPYRNSLRKAHIFGTTSFQAMMYESIACP 957
 QY 961 RFGAYLAHSLSMSPDVLLVFSAVFGAMAVQVSPPADYAKAVSAAHIMIETPL 1020
 DB 958 RFGAYLAHKLMSPDVLLVFSAVFGAMAVQVSPPADYAKKISAHIMIETPL 1017
 DB 1021 IDSYSTEGLKPNTLLEGNTVNEVVFNYPRLDIPVLOGLSLEYKGOTIALVGSSGCCRS 1080
 QY 1018 IDSYSTEGLMPNTLLEGNTVGEVVFNYPRPDIPVLOGLSLEYKGOTIALVGSSGCCRS 1077
 QY 1081 TVVOLLERFDPLAKVUJLGDKEIKOLNQWLPBLGIYQSOPPLFDCSISENIALYGENS 1140
 DB 1078 TVVQLLERFDPLAKVUJLGDKEIKLNQWLPBLGIYQSOPPLFDCSIAENIAYGENS 1137
 QY 1141 RVVSQEETVRAAEANTHPIESLPLNOSTRIVEDKGTKQSLGGOKQRIARALYRPHL 1200
 DB 1138 RVVSQEETVRAAEANTHPIESLPLNOSTRIVEDKGTKQSLGGOKQRIARALYRPHL 1197
 DB 1201 LLDEATSALDTESEKVKOYALDKAREGRCTCIVIAHRLSTIONADLIVVFGNGVKERCH 1260
 DB 1198 LLDEATSALDTESEKVKOYALDKAREGRCTCIVIAHRLSTIONADLIVVFGNGVKERCH 1257
 QY 1261 QOLLAOKGIXFSNVSYOAGAKRQ 1283
 DB 1258 QOLLAOKGIXFSNVSYOAGAKRQ 1280
 QY 1281 ATINGGLOPAFAVIFSKIGIFTRNDDAETKRQNSNLPSLLPLVGLIVSPITFFLOGFTF 780
 ; APPLICANT: Bunting, Kevin
 ; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 ; METHODS OF USE THEREOF
 ; FILE REFERENCE: 1340-1-021CIP
 ; CURRENT APPLICATION NUMBER: US/09/584,586
 ; EARLIER APPLICATION NUMBER: US 60/086,988
 ; EARLIER FILING DATE: 1988-05-28
 ; EARLIER APPLICATION NUMBER: PCT/US99/11825
 ; EARLIER FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 4
 ; LENGTH: 1280
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Human MDR 185-V
 ; US-09-584-586-4
 Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
 Qy 1 MDLEGDRNGGAEKNNFKLANNKSKDQKERKERTPVTSFSMFRYSNWLDKLYMVGTLLAI 60
 Db 1 MDLEGDRNGGAEKNNFKLANNKSKDQKERKERTPVTSFSMFRYSNWLDKLYMVGTLLAI 60
 Qy 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNNTSSNIDTVPYMNLERDMTRVAY 120
 Db 61 HGAGLPLMLVFGDMTDIFANAGNLGDLGALLFNNNTSSNIDTVPYMNLERDMTRVAY 117
 Qy 121 YSGTAGVLUAVIATQVSTWCLAGROTHKIRKOFFAHMROPIGWVHDVGELENRLTD 180
 Db 118 YSGTAGVLUAVIATQVSTWCLAGROTHKIRKOFFAHMROPIGWVHDVGELENRLTD 177
 Qy 181 DYSRINEGIGDKGMMFFOSMATEFTGFIVGFTTRGMKLTIVLVAISPVTLGSSAWAKILS 240
 Db 178 DVSKINEVIGDKGMMFFOSMATEFTGFIVGFTTRGMKLTIVLVAISPVTLGSSAWAKILS 237
 Qy 241 SFDTKELLAYAKGAVAEVLAIRTYTAFGQKKELERYNKLNLEAKRIGTKKATANI 300
 Db 238 SFDTKELLAYAKGAVAEVLAIRTYTAFGQKKELERYNKLNLEAKRIGTKKATANI 297
 Qy 301 SIGAELLIYASALAFAYGCTTIVLSEKEYSISQVLTVEFSLIGAFSYQASPSIARAN 360
 Db 298 SIGRAELLIYASALAFAYGCTTIVLSEKEYSISQVLTVEFSLIGAFSYQASPSIARAN 357
 Qy 361 ARGNAEFLPKIDNPKSDSYSKSGHPDNIGKLNLPBNHESYPSKEKEVKKLKGNLKV 420
 Db 358 ARGNAEFLPKIDNPKSDSYSKSGHPDNIGKLNLPBNHESYPSKEKEVKKLKGNLKV 417
 Qy 421 QSGOTVALVGNSCCGKSTTQVLMQRLYDPTGMSVSDGDIRTIVRLREITIVGSQEP 480
 Db 418 QSQQTVALVGNSCCGKSTTQVLMQRLYDPTGMSVSDGDIRTIVRLREITIVGSQEP 477
 Qy 541 RIAJARALYRNPKILLDEATSALDTESEAVQVALIDKARGCRITIVIAHRLSTVNADV 600
 Db 538 RIAJARALYRNPKILLDEATSALDTESEAVQVALIDKARGCRITIVIAHRLSTVNADV 597
 Qy 601 TAGFDDEVIVEGNHDELMKKGKSYGRNTMDIEKAKEANAYDFIMKLPKFDTLYGERGAQLSGGQK 540
 Db 478 VLFATTAAENITYGREDTMDEIEKAKEANAYDFIMKLPKFDTLYGERGAQLSGGQK 537
 Qy 598 TAGFDGIVTEGHNHDLMKKGKSYGRNTMDIEKAKEANAYDFIMKLPKFDTLYGERGAQLSGGQK 657
 Qy 661 SGSSLIRKRSRSPRSVGSQGDRKSTKEALDESIPVSFRIMKLNLTFENDYFVGVC 720
 Qy 658 SRSSLIRKRSRSPRSVGSQGDRKSTKEALDESIPVSFRIMKLNLTFENDYFVGVC 717
 ; CENTRAL INFORMATION:
 ; INVENTOR: Sorrentino, Brian

RESULT 12
US-09-584-586-4Sequence 4, Application US/09/84586
Patent No. 6933150CENTRAL INFORMATION:
INVENTOR: Sorrentino, Brian

Query Match	96.6% ; Score 6209; DB 2; Length 1280;	Db	1021 YSTEGLKPNTLEGNVTPRDLIFVQLGSLIEVKKGQTIALVGSSGGKSTVV 1080
Best Local Similarity	96.6% ; Pred. No. 0;	Qy	1081 QLLEFRYDPLAKVLLDGKEIKOLNQWMLRAHILGIVSQEPLFDPSIENIAYGNSRVV 1140
Matches 1236 ; Conservative	19; Mismatches 25; Indels 0; Gaps 0;	Db	1081 QLLEFRYDPLAKVLLDGKEIKOLNQWMLRAHILGIVSQEPLFDPSIENIAYGNSRVV 1140
Qy	1 MDLEGDRNGGAKKNPKLNKSKDKCKRERKPTVSYSMFRYSNWLKDLYMVGTAAII 60	Db	1141 SQEEFVRAAKEANTHAFILESPNPKYSTRVEDKGTLGGOKORIAJARALYRQPHILLD 1200
Db	1 MDLEGDRNGGAKKNPKLNKSKDKCKRERKPTVSYSMFRYSNWLKDLYMVGTAAII 60	Qy	1141 SQEEFVRAAKEANTHAFILESPNPKYSTRVEDKGTLGGOKORIAJARALYRQPHILLD 1200
Qy	61 HGAGLPMMLVFGDMTDTPANAGYICD/GALLTNSNTITPVYNNLEIMTRYAYYYSG 120	Db	1141 SQEEFVRAAKEANTHAFILESPNPKYSTRVEDKGTLGGOKORIAJARALYRQPHILLD 1200
Db	61 HGAGLPMMLVFGEMTDIFANAGNLEDLMNSITNRDINDGFFWNLDEIMTRYAYYYSG 120	Qy	1201 EATSLDTESEKVKYOBALDKAREGTCIVIAHRLSTIONADLVFQNGRKVEHGTHQOL 1260
Qy	121 IGGVLUVAVIATQVSFCIAGAOIHKTRKQPHAMRQEIGWDFHDVGELENTRDDVS 180	Db	1201 EATSLDTESEKVKYOBALDKAREGTCIVIAHRLSTIONADLVFQNGRKVEHGTHQOL 1260
Db	121 IGGVLUVAVIATQVSFCIAGAOIHKTRKQPHAMRQEIGWDFHDVGELENTRDDVS 180	Qy	1261 LAQRGTYFSMVSYQGAKRQ 1280
Qy	181 KINEGIGDKIGMFQSMATFTGFIYGFTRQWLKLTVILAIASPVUGLSAAWAKLSSFT 240	Db	1261 LAQRGTYFSMVSYQGAKRQ 1280
Db	181 KINEGIGDKIGMFQSMATFTGFIYGFTRQWLKLTVILAIASPVUGLSAAWAKLSSFT 240	Qy	RESULT 11. US-09-817-762-3
Qy	241 DKEILAYAKAGAVAREVLAIRTVIAFGGOKKELPERYKNULEAKRIGKKAITAATNISIG 300	Db	; Application US/09817762
Db	241 DKEILAYAKAGAVAREVLAIRTVIAFGGOKKELPERYKNULEAKRIGKKAITAATNISIG 300	Qy	; Sequence No. 6858774
Qy	301 AAFLITYASALAFWNGTFLVLSKEYSIGVQLTVFVSLICAFPSVQASPSIEAPANARG 360	Db	; GENERAL INFORMATION:
Db	301 AAFLITYASALAFWNGTFLVLSKEYSIGVQLTVFVSLICAFPSVQASPSIEAPANARG 360	Qy	; APPLICANT: Spalding, Edgar P.
Qy	361 AAEIFPKIIDKPKPSIDSYSKSGHKPDTNICKNLEFRNHFSYPSRKEVKLURGLNLKVQSG 420	Db	; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
Db	361 AAEIFPKIIDKPKPSIDSYSKSGHKPDTNICKNLEFRNHFSYPSRKEVKLURGLNLKVQSG 420	Qy	; APPLICANT: No. 6858774, Bosl
Qy	421 QTVALVGNSSCGKSTSIVQLMORLYDTEGMVSYDGDIDRTINVRFLREITGVYVSQRPVLF 480	Db	; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
Db	421 QTVALVGNSSCGKSTSIVQLMORLYDTEGMVSYDGDIDRTINVRFLREITGVYVSQRPVLF 480	Qy	; FILE REFERENCE: 13238-00061
Qy	481 ATTIAENTRYGREDTMDTEIKAKEVANADFIMKLPOKEPDITLGVERGAQLSGGOKORIA 540	Db	; CURRENT APPLICATION NUMBER: US/09-817,762
Db	481 ATTIAENTRYGRENTMDTEIKAKEVANADFIMKLPHKDITLGVERGAQLSGGOKORIA 540	Qy	; PRIORITY FILING DATE: 2005-03-26
Qy	541 TARALYRNPKIILDEATSALDTESEAVQVALDKARKRGTIVIAHRLSTVRNAVIDAG 600	Db	; PRIOR APPLICATION NUMBER: PCT/US99/22363
Db	541 TARALYRNPKIILDEATSALDTESEAVQVALDKARKRGTIVIAHRLSTVRNAVIDAG 600	Qy	; PRIORITY FILING DATE: 1999-06-24
Qy	601 FDDGVIVEKENHDELMKEKGTYFKLVTMTQAGNEIENLADESIETDLEMSSHDSS 660	Db	; NUMBER OF SEQ ID NOS: 14
Db	601 FDDGVIVEKENHDELMKEKGTYFKLVTMTQAGNEIENLADESIETDLEMSSHDSS 660	Qy	; SOFTWARE: FastSEQ for Windows Version 4.0
Qy	661 SLIRKRSSTRSVRGSGQDRLKSLTEBALDESIPPFSWRIMKLNLTEPVFVGFCII 720	Db	; SEQ ID NO: 3
Db	661 SLIRKRSSTRSVRGSGQDRLKSLTEBALDESIPPFSWRIMKLNLTEPVFVGFCII 720	Qy	; LENGTH: 1280
Qy	721 NGGLOPAFVIFSKLIGIFTENDDAETKRQNSNLFLFLVGLIVSFITFLQGFTFGKA 780	Db	; TYPE: PRT
Db	721 NGGLOPAFVIFSKLIGIFTENDDAETKRQNSNLFLFLVGLIVSFITFLQGFTFGKA 780	Qy	; ORGANISM: Homo sapiens
Qy	781 GEITTKPLRYMVERSMRQDSWDFDPKNTGTLRNLDAQYKGAIGSRLAITONI 840	Db	; PUBLICATON INFORMATION:
Db	781 GEITTKPLRYMVERSMRQDSWDFDPKNTGTLRNLDAQYKGAIGSRLAITONI 840	Qy	; DATABASE ACCESSION NUMBER: Genbank P08183
Qy	841 ANLGPGLIISLJYGHQTLLLAIAPLIAQYVEMKMSQAQDKELEGAKTATEA 900	Db	; DATABASE ENTRY DATE: 1997-11-01
Db	841 ANLGPGLIISLJYGHQTLLLAIAPLIAQYVEMKMSQAQDKELEGAKTATEA 900	Qy	; US-09-817-762-3
Qy	901 IENFRITVSLTOEQKFPEHMYDQSLOVYPRNSLRKAHIFGITESFOAMMFSYAGCERFG 960	Db	; LENGTH: 1280;
Db	901 IENFRITVSLTOEQKFPEHMYDQSLOVYPRNSLRKAHIFGITESFOAMMFSYAGCERFG 960	Qy	; Best Local Similarity 96.6%; Pred. No. 0; Mismatches 25; Indels 0; Gaps 0;
Qy	961 AYLVAHKLMSPFDVLIVSAVEGAMAVQSSPADYAKAVSAAHIMLIEKTPLIDS 1020	Db	1 MDLEGDRNGGAEKKNPKLNKSKDKCKRERKPTVSFSMFRYSNWLKLYMVVGTLAAII 60
Db	961 AYLVAHKLMSPFDVLIVSAVEGAMAVQSSPADYAKAVSAAHIMLIEKTPLIDS 1020	Qy	1 MDLEGDRNGGAEKKNPKLNKSKDKCKRERKPTVSFSMFRYSNWLKLYMVVGTLAAII 60
Qy	1021 YSTEGLKPNTLEGNVTPRDLIFVQLGSLIEVKKGQTIALVGSSGGKSTVV 1080	Db	61 HGAGLPMLVFGDNMTDPANAGNJDGALLTNSSNITDTPVNLNEDDMTRIAYYYSG 120
Qy		Db	61 HGAGLPMLVFGDNMTDPANAGNJDGALLTNSSNITDTPVNLNEDDMTRIAYYYSG 120
Qy		Qy	121 IGAGTVAAATQVSPWCLAAQROIKIRKOFFHAIRMROEIGWFDVHVGELNTRDDVS 180
Db		Db	121 IGAGTVAAATQVSPWCLAAQROIKIRKOFFHAIRMROEIGWFDVHVGELNTRDDVS 180
Qy		Qy	121 IGAGTVAAATQVSPWCLAAQROIKIRKOFFHAIRMROEIGWFDVHVGELNTRDDVS 180
Db		Db	121 IGAGTVAAATQVSPWCLAAQROIKIRKOFFHAIRMROEIGWFDVHVGELNTRDDVS 180
Qy		Qy	181 KINEGIGDKIGMFQPSMATEFTGFTVGFTRGKLTIVLIAISPVGLSAAWAKLSSFT 240
Db		Db	181 KINEGIGDKIGMFQPSMATEFTGFTVGFTRGKLTIVLIAISPVGLSAAWAKLSSFT 240
Qy		Qy	241 DKEILAYAKAGAVAREVLAIRTVIAFGGOKKELPERYKNULEAKRIGKKAITAATNISIG 300
Db		Db	241 DKEILAYAKAGAVAREVLAIRTVIAFGGOKKELPERYKNULEAKRIGKKAITAATNISIG 300
Qy		Qy	301 AAFLIYAYASALAFYGTTLVLSKEYSISGYOLTYFVSLIGAFSYQASPSIBAFANARG 360

3.01 AAFLLIYASAYALAFWYGTIVLVLSEGEYSIGQVLTIVPFSVQASPSIEAFANARG 360
 3.61 AAFELPKIINPKPSIDSYSKSGHKPKNIKGKLEFRNIVHFSYPSREVKLKGLNKLVQSG 420
 3.61 AAYELPKIINPKPSIDSYSKSGHKPKNIKGKLEFRNIVHFSYPSREVKLKGLNKLVQSG 420
 4.21 QTVALVGNSGGKSTTVQLMORLYDPTBGMSVSDGDIRTINVRFLRETLGVVSOEPVLF 480
 4.21 QTVALVGNSGGKSTTVQLMORLYDPTBGMSVSDGDIRTINVRFLRETLGVVSOEPVLF 480
 4.81 ATTIAENIRYGRDNTMDEIKAVERANAYDFIMKLPOKEDTLVGERAQLGGOKORA 540
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 54.1 TARALVNPCKLILLDEATSAUDTESSAVQVALDKARKRITIVAHRLSTVRADIVAG 600
 54.1 TARALVNPCKLILLDEATSAUDTESSAVQVALDKARKRITIVAHRLSTVRADIVAG 600
 60.1 FDDGVIVEKGHNHDELMKEKGTYFKLVMTMOPAGNEBLENDADESKEEITLLEMSSHDSS 660
 60.1 FDDGVIVEKGHNHDELMKEKGTYFKLVMTMOPAGNEBLENDADESKEEITLLEMSSHDSS 660
 66.1 SLIRKRSTRSRYSGSQODRKLSSTEALDESIPPFSWRIMKLNITEWPMVPGYFCATTI 720
 66.1 SLIRKRSTRSRYSGSQODRKLSSTEALDESIPPFSWRIMKLNITEWPMVPGYFCATTI 720
 72.1 NGGLQPAFVFSKIGITFTNDDAETKTRONSNLPSLFLVLGIVSFITPLQGFTFGA 780
 72.1 NGGLQPAFVFSKIGITFTNDDAETKTRONSNLPSLFLVLGIVSFITPLQGFTFGA 780
 78.1 GEILTLTRKLYMFVRSMLRDQYSWFDPPKTGALTRLANDAAOTKGAGSRLAITONTI 840
 78.1 GEILTLTRKLYMFVRSMLRDQYSWFDPPKTGALTRLANDAAOTKGAGSRLAITONTI 840
 78.1 GEILTLTRKLYMFVRSMLRDQYSWFDPPKTGALTRLANDAAOTKGAGSRLAITONTI 840
 78.1 GEILTLTRKLYMFVRSMLRDQYSWFDPPKTGALTRLANDAAOTKGAGSRLAITONTI 840
 84.1 ANLGTGIIISIYGMQLTLLIAIYPIIATAGVEMKMSQALDKDKELEGAKIATEA 900
 84.1 ANLGTGIIISIYGMQLTLLIAIYPIIATAGVEMKMSQALDKDKELEGAKIATEA 900
 90.1 IENFRITVSIHQFHEHYDOSQPYRNSLRAHQFVQGAGSRLAVTONI 960
 90.1 IENFRITVSIHQFHEHYDOSQPYRNSLRAHQFVQGAGSRLAVTONI 960
 96.1 AYLVAHSLMSPEVDLIVPSAVVFGAMAVGQVSSFAPDYZAKVSAAHIMIIEKPLIDS 1020
 96.1 AYLVAHSLMSPEVDLIVPSAVVFGAMAVGQVSSFAPDYZAKVSAAHIMIIEKPLIDS 1020
 96.1 AYLVAHSLMSPEVDLIVPSAVVFGAMAVGQVSSFAPDYZAKVSAAHIMIIEKPLIDS 1020
 102.1 YSTEGLKPNTLEGNTFNEYVNFYPTPLDIPVQSLISLEYKGCTLATVGSGGKSTVV 1080
 102.1 YSTEGLKPNTLEGNTFNEYVNFYPTPLDIPVQSLISLEYKGCTLATVGSGGKSTVV 1080
 108.1 OLLERFYDPLAKVLDGEIKLQINQWLAHLGIVSQEPILFDISIENIAGNDSRV 1140
 108.1 OLLERFYDPLAKVLDGEIKLQINQWLAHLGIVSQEPILFDISIENIAGNDSRV 1140
 114.1 SQEEIVRAKEANTHIAFILESPNCKSTRVGDKGTLPSGOKRITATARALVROPHILLID 1200
 114.1 SQEEIVRAKEANTHIAFILESPNCKSTRVGDKGTLPSGOKRITATARALVROPHILLID 1200
 120.1 EATSALDTESEKYYVQBALDKAREGRITCIVTAHRLSTIQNADLIVYFQNQRYKEHGTHQOL 1260
 120.1 EATSALDTESEKYYVQBALDKAREGRITCIVTAHRLSTIQNADLIVYFQNQRYKEHGTHQOL 1260
 126.1 LAQKCYFMSVQGARQ 1280
 126.1 LAQKCYFMSVQGARQ 1280
 RESULT 12
 US-09-584-586-4
 Sequence 4, Application US/09584586
 Patent No: 6933110
 GENERAL INFORMATION:
 APPLICANT: Sorrentino, Brian

721 NGGLQPAFAIFSKIGVTRIDDPETRQNSNLFSLFLAIGIISITFFLQGFEGKA 780
 781 GBLTKRLRYMERSMRQDSWDDPNTGSAITTLANDAQVKAIGSRLAVITQNI 840
 781 GBLTKRLRYMERSMRQDSWDDPNTGSAITTLANDAQVKAIGSRLAVITQNI 840
 841 ANLGTGIIISLIGWQTTLLIAIVPIAIGVEMMLSGALDKKELGAGKATEA 900
 841 ANLGTGIIISLIGWQTTLLIAIVPIAIGVEMMLSGALDKKELGAGKATEA 900
 901 IENFRTVSLTQEQPEHMTDOSLQVPRYNSLRKAHTFGITFSPTOAMMFSYAGCERFG 960
 901 IENFRTVSLTQEQPEHMTDOSLQVPRYNSLRKAHTFGITFSPTOAMMFSYAGCERFG 960
 961 AYLVAHSLMSPEEDVLLVSAVYFGAMAQGYSSRFADPYAKVSAAHIMIETPLIDS 1020
 961 AYLVAHSLMSPEEDVLLVSAVYFGAMAQGYSSRFADPYAKVSAAHIMIETPLIDS 1020
 1021 YSTEGLKPNTELEGNTTPNEVUNYPTRLDPVQLGISELEVKGOTPLVGSGCCGSTVV 1080
 1021 YSTEGLKPNTELEGNTTPNEVUNYPTRLDPVQLGISELEVKGOTPLVGSGCCGSTVV 1080
 1081 QLERFPYDPLAGKVLLDGEIKQKLNQWIRAHLGIVSQEPILFDCSISENIAYGDNSRVV 1140
 1081 QLERFPYDPLAGKVLLDGEIKQKLNQWIRAHLGIVSQEPILFDCSISENIAYGDNSRVV 1140
 1141 SQEETVRAKEANTHAFTISLPLNKSYSTRVGDKGFLPSQKOKTAIRALVRPHILLID 1200
 1141 SQEETVRAKEANTHAFTISLPLNKSYSTRVGDKGFLPSQKOKTAIRALVRPHILLID 1200
 1201 EATSDLTESRKVYQEALKAREERTCTVIAHRUSTINQADLTVFQNGRVKEHGHQQL 1260
 1201 EATSDLTESRKVYQEALKAREERTCTVIAHRUSTINQADLTVFQNGRVKEHGHQQL 1260
 1261 LAQKGIYSMMSVYQAGKQ 1280
 1261 LAQKGIYSMMSVYQAGKQ 1280

RESULT 13
 US-08-583-276-19
 Sequence 19, Application US/08583276
 Patent No. 587536
 GENERAL INFORMATION:
 APPLICANT: McDonagh, Kevin T.
 APPLICANT: Nienhuis, Arthur
 APPLICANT: Tolstoshev, Paul
 ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
 TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
 MULTIDRUG RESISTANCE GENES AND IMPROVED
 TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 CARELLA, BYRNE, BAIN, GILFILLAN,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 COMPUTER: IBM PS/2
 SOFTWARE: DW4_V2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/583,276
 FILING DATE: 05-JAN-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/332,444
 FILING DATE: 31-OCT-1994
 APPLICATION NUMBER: 07/887,712

FILING DATE: 22-MAY-1992
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1280 amino acids
 TYPE: amino acid
 STRANDBENESS:
 MOLECULE TYPE: linear
 DESCRIPTION: protein
 US-08-583-276-19

Query	Match	Score	DB	Length	
	96.6%	6206;	1;	1280;	
	96.5%	96.5%;	0;	0;	
	Conservative	20;	Mismatches	0;	
	Matches Local	96.5%;	Indels	0;	
	1235;		Gaps	0;	
Qy	1	MDLGDGRNGAEXKCNFFKLNKSKCKKCKPVTFSMFRYSNWLDKLYMVGTLLAII 60	Db	1	MDLGDGRNGAEXKCNFFKLNKSKCKKCKPVTFSMFRYSNWLDKLYMVGTLLAII 60
Qy	61	HGAGLPLMLVPGMTDTPANAGNLGDLGALLTNSSNITDTVPVMNLBEDMTRYAYYSG 120	Db	61	HGAGLPLMLVPGMTDTPANAGNLGDLGALLTNSSNITDTVPVMNLBEDMTRYAYYSG 120
Qy	121	IGAGVLVAYIYQVSFWCLAAGROHKIRKOPFHAIMROBIGNFDHDVGELETTRTDVY 180	Db	121	IGAGVLVAYIYQVSFWCLAAGROHKIRKOPFHAIMROBIGNFDHDVGELETTRTDVY 180
Qy	181	KINGIGDKGKIGMFQSMATTEFFGIVGFTGRWKFLTVLIAISPVLGISAAWAKILSSFT 240	Db	181	KINGIGDKGKIGMFQSMATTEFFGIVGFTGRWKFLTVLIAISPVLGISAAWAKILSSFT 240
Qy	241	DKEILAYAKAGVAYEVLAIAKTVIAFGQQKKELEERYKNUBEAKRIGKCAITANISIG 300	Db	241	DKEILAYAKAGVAYEVLAIAKTVIAFGQQKKELEERYKNUBEAKRIGKCAITANISIG 300
Qy	301	AAFLLYASYALAFWGTGTTVLSKEYSIGVOLTVFPLSVLGAFTSYGQASPIEAFANARG 360	Db	301	AAFLLYASYALAFWGTGTTVLSKEYSIGVOLTVFPLSVLGAFTSYGQASPIEAFANARG 360
Qy	361	AAFEIIFKLIDNKPSPDSYSKSGHKPDNKENLEFRVNHFESYPSREKEVKLKGLNLKVQSG 420	Db	361	AAFEIIFKLIDNKPSPDSYSKSGHKPDNKENLEFRVNHFESYPSREKEVKLKGLNLKVQSG 420
Qy	421	QTVALVGNSGGKSKSTVOLMQRLYDPTEGMVSVDQDIRTINVPLREIIGVVSSEPVPLV 480	Db	421	QTVALVGNSGGKSKSTVOLMQRLYDPTEGMVSVDQDIRTINVPLREIIGVVSSEPVPLV 480
Qy	481	ATTIAENIRYGREDTTMDELEKAYEANAYDFIMLPLQEKDTLVGERGAQLSGGKQORIA 540	Db	481	ATTIAENIRYGREDTTMDELEKAYEANAYDFIMLPLQEKDTLVGERGAQLSGGKQORIA 540
Qy	541	IRALAVRNPKLILLDEATSALDTESEAVYQVALDKARKGRTTIVIAHRSITVNAADVAG 600	Db	541	IRALAVRNPKLILLDEATSALDTESEAVYQVALDKARKGRTTIVIAHRSITVNAADVAG 600
Qy	601	FDDGVIVEKGNHDELMKKGCIYFKLVTNOTAGBEILENAADESKEIDLTEMSHSDSGS 660	Db	601	FDDGVIVEKGNHDELMKKGCIYFKLVTNOTAGBEILENAADESKEIDLTEMSHSDSGS 660
Qy	661	SLIRKRSTRSFRSVEQSQGDRKLSTKEALDESIPPSWRIMKLNLTENPYFVGFCAII 720	Db	661	SLIRKRSTRSFRSVEQSQGDRKLSTKEALDESIPPSWRIMKLNLTENPYFVGFCAII 720
Qy	721	NGGLQPAFVIFSKIGITFRNDDAETKRONSNLFSLFLVGLGIVSPTTFLOGPTFGKA 780	Db	721	NGGLQPAFVIFSKIGITFRNDDAETKRONSNLFSLFLVGLGIVSPTTFLOGPTFGKA 780
Qy	781	GEILTKRLRYMFRSMIIRDQVSNFDPNTGALTTRIANDAQVKGAGIGSRILAITTONI 840	Db	781	GEILTKRLRYMFRSMIIRDQVSNFDPNTGALTTRIANDAQVKGAGIGSRILAITTONI 840
Qy	841	ANLGTGIIISLIGWQWTLLAIAVPIAIGVEMMLSGQLDKKELGAGKATEA 900	Db	841	ANLGTGIIISLIGWQWTLLAIAVPIAIGVEMMLSGQLDKKELGAGKATEA 900

Db	841. ANLGTGIIISPIYGWQLTLLAIVPIIAIGVVMKMSQALKDKKELEGAGKIAEA 900	Db	241 DKELLAYAKAGAAVEVLAIAIRTVIAGGGOKKELEERYNKNLBEEAKRIGIKKAITANISIG 300
Qy	901. IENFRTVVSLTOEQPKERMYDQS1QVPPNSLREAHIFGITESTPQAMMFYSTAGCFFRG 960	Qy	301 AAPLTITASYLAFWYGTPLTISKEYTIGQVLTIVF5VLGAFPSVGASPSLEAFNARG 360
Db	901. IENFRTVVSLTOEQPKERMYDQS1QVPPNSLREAHIFGITESTPQAMMFYSTAGCFFRG 960	Db	301 AAPLTITASYLAFWYGTPLTISKEYTIGQVLTIVF5VLGAFPSVGASPSLEAFNARG 360
Qy	961. AYLVAHSIAMSPEDVLLVPSAVVFGAMAIVQVSSPAPDYAKAIVSAAHIMIIEKTPLIDS 1020	Qy	361 AAPBKLIIDNKPDSIDSYSKSGKPKDNIKGNEFRVHFSYPSRKKEYTIGQVLTIVF5VLGAFPSVGASPSLEAFNARG 420
Db	961. AYLVAHKLMSPEDVLLVPSAVVFGAMAIVQVSSPAPDYAKAIVSAAHIMIIEKTPLIDS 1020	Db	361 AAPBKLIIDNKPDSIDSYSKSGKPKDNIKGNEFRVHFSYPSRKKEYTIGQVLTIVF5VLGAFPSVGASPSLEAFNARG 420
Qy	1021. YSTEGGLKPTNLEGNVTFNENVFNYPTRDIPVULGSLSEVKKGOTLALVSSCGKSTVV 1080	Qy	421 OTVALVGNSGCCGSTVQMLQRYDPTEGMYSVDDGDIRTINVRFLREIIGVVSQEPVLF 480
Db	1021. YSTEGGLMPTNLEGNVTFGTEVNFYNTFPTRDIPVULGSLSEVKKGOTLALVSSCGKSTVV 1080	Db	421 OTVALVGNSGCCGSTVQMLQRYDPTEGMYSVDDGDIRTINVRFLREIIGVVSQEPVLF 480
Qy	1081. QLLRFYDPLAKVLLDGEBIKQLNQVWRHLGIVSOPDILFCISIHNIAIGDNSRV 1140	Qy	481 ATTIAENTRYGEDVTMDEIEKAVKEANAYDFMCLMOKFDTLVGERAQLSGGOKORIA 540
Db	1081. QLLRFYDPLAKVLLDGEBIKQLNQVWRHLGIVSOPDILFCISIHNIAIGDNSRV 1140	Db	481 ATTIAENTRYGREENVTMDEIEKAVKEANAYDFMCLMOKFDTLVGERAQLSGGOKORIA 540
Qy	1141. SOEELVRAKEANIAHFBSLPNKYSTVGDKGCTOLSGGOKORTAIARALVROPHILLID 1200	Qy	541 TAPALVNPKILLDEATSALDTESEAVVQVALDKARKGRRTIVIAHRLSTYRNADYTAG 600
Db	1141. SOEELVRAKEANIAHFBSLPNKYSTVGDKGCTOLSGGOKORTAIARALVROPHILLID 1200	Db	541 TAPALVNPKILLDEATSALDTESEAVVQVALDKARKGRRTIVIAHRLSTYRNADYTAG 600
Qy	1201. EATSLADTSEKVVOBALLDAREGRTCIVIAHRLSTIONADLIVVQNGRVKEHGTHCOL 1260	Qy	601 FDDCVIVEKGNHDLMKEKG1YPKLJTMOTAGNEELENDAEDESSTDLEMSSHDGS 660
Db	1201. EATSLADTSEKVVOBALLDAREGRTCIVIAHRLSTIONADLIVVQNGRVKEHGTHCOL 1260	Db	601 FDDCVIVEKGNHDLMKEKG1YFKLJTMOTAGNEELENDAEDESSTDLEMSSHDGS 660
Qy	1261 LAQKGIYFMSVYORGAKRQ 1280	Qy	661 SLIRKRSTRSRSYSGQADRKLSTEAKADESIPPVSFRIMKLNTEPYFVGFCAII 720
Db	1261 LAQKGIYFMSVYORGAKRQ 1280	Db	661 SLIRKRSTRSRSYSGQADRKLSTEAKADESIPPVSFRIMKLNTEPYFVGFCAII 720
<hr/>			
Qy	RESULT 14	Qy	721 NGGLQPAFVFSKIGIIFTTRNDAEKTRONSNFLSILFLVLGIVSFITFFLOGFTFKKA 780
Db	526352-4	Db	721 NGGLQPAFVFSKIGIIFTTRNDAEKTRONSNFLSILFLVLGIVSFITFFLOGFTFKKA 780
; Patent No. 5206352		Qy	781 GEILTKEURYMPMSLQDVSFEDPKNTGALTTRLANDAQVKGAIGSRALITONI 840
; APPLICANT: Robinson, Igor B.; Pastan Ira H.; Gotteman, Michael M.		Db	781 GEILTKEURYMPMSLQDVSFEDPKNTGALTTRLANDAQVKGAIGSRALITONI 840
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA		Qy	841 ANLGTGIIISLIGWQLTLLAIVPIIAIGVEMNLSGQALKDKELEGAKIATEA 900
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS		Db	841 ANLGTGIIISLIGWQLTLLAIVPIIAIGVEMNLSGQALKDKELEGAKIATEA 900
; NUMBER OF SEQUENCES: 4		Qy	901 IBNFRTVVSLTOEQPKERMYDQSLOQPVYRNSLRKAHFGITISFTOMAMYFSYAGCRFG 960
; CURRENT APPLICATION DATA:		Db	901 IBNFRTVVSLTOEQPKERMYDQSLOQPVYRNSLRKAHFGITISFTOMAMYFSYAGCRFG 960
; APPLICATION NUMBER: US/07/622, 836		Qy	961 AYLVAHSLMSFEDVLLVPSAVVFGAMAIVQVSSFADPYAKAIVSAAHIMIETKPLIDS 1020
; FILING DATE: 24-SEP-1990		Db	961 AYLVAHSLMSFEDVLLVPSAVVFGAMAIVQVSSFADPYAKAIVSAAHIMIETKPLIDS 1020
; PRIOR APPLICATION DATA:		Qy	1021 YSTEGLKENTLEGTVTFREVWVTPTRDIPLOGSLEVKKGOTLALVGSSCGKSTVV 1080
; APPLICATION NUMBER: 892, 575		Db	1021 YSTEGLKENTLEGTVTFREVWVTPTRDIPLOGSLEVKKGOTLALVGSSCGKSTVV 1080
; FILING DATE: 01-AUG-1986		Qy	1081 QLIERFYDELAGKVLDGEKEIKOUNVOMVRAHIGIVSVBPLFDCISBNIAYGDNSRVV 1140
; SEQ ID NO: 4;		Db	1081 QLIERFYDELAGKVLDGEKEIKOUNVOMVRAHIGIVSVBPLFDCISBNIAYGDNSRVV 1140
; LENGTH: 1280		Qy	1141 SOBERTRAKEANTHAFALESPLPKYSTRVGDGTQTSQGOKORIAJARALVROPHILLID 1200
526352-4		Db	1141 SOBERTRAKEANTHAFALESPLPKYSTRVGDGTQTSQGOKORIAJARALVROPHILLID 1200
Query Match 96.6%; Score 6206; DB 7; Length 1280;		Qy	1141 SOBERTRAKEANTHAFALESPLPKYSTRVGDGTQTSQGOKORIAJARALVROPHILLID 1200
Best Local Similarity 96.5%; Pred. No. 0;		Db	1141 SOBERTRAKEANTHAFALESPLPKYSTRVGDGTQTSQGOKORIAJARALVROPHILLID 1200
Matches 1235; Conservative 20; Mismatches 0; Indels 0;		Db	1201 EATSLADTSEKVVOBALLDAREGRTCIVIAHRLSTIONADLIVVQNGRVKEHGTHCOL 1260
Qy 1. MDLEGDRNGAELKONPKRANKSKCDKEKEKPTYSVSMPPRSYNTWLDKLYMNYCTLAII 60		Db	1201 EATSLADTSEKVVOBALLDAREGRTCIVIAHRLSTIONADLIVVQNGRVKEHGTHCOL 1260
Db 1. MDLEGDRNGAELKONPKRANKSKCDKEKEKPTYSVSMPPRSYNTWLDKLYMNYCTLAII 60		Qy	1211 IGGVLYVAATIQVSPWCLAAQRQTHKIRKOFFHAIMRQEIGWFDYHVDGELNTRLTDYVS 180
Qy 61. HGAGIPLMLVFLVGFEMDTFANAGNGLDGAIIITNSNITDTPVNMLEDMDTRAYYSG 120		Db	1211 HGAGIPLMLVFLVGFEMDTFANAGNGLDGAIIITNSNITDTPVNMLEDMDTRAYYSG 120
Db 61. HGAGIPLMLVFLVGFEMDTFANAGNLEDLMSNTINESDINTGFFANLEDMDTRAYYSG 120		Qy	1211 IGGVLYVAATIQVSPWCLAAQRQTHKIRKOFFHAIMRQEIGWFDYHVDGELNTRLTDYVS 180
Qy 181. KINEGIGD1KGMFFQSMATPTGFYVGFTGWLTKLVLLISPLGLSAAWAKLSSPT 240		Db	1211 KINEGIGD1KGMFFQSMATPTGFYVGFTGWLTKLVLLISPLGLSAAWAKLSSPT 240
Db 181. KINQVGD1KGMFFQSMATPTGFYVGFTGWLTKLVLLISPLGLSAAWAKLSSPT 240		Qy	1261 LAQKGIYFMSVYOGAKRQ 1280
Qy 241. DKELLAYAKAGAAVEVLAIAIRTVIAGGGOKKELEERYNKNLBEEAKRIGIKKAITANISIG 300		Db	1261 LAQKGIYFMSVYOGAKRQ 1280

1 MDLERDRNGGAEKKFKLANKSKDKKERKPTVSFMSFRYSWLDKLYMVVETLAATI 60
 1 MDLERDRNGGAEKKFKLANKSKDKKERKPTVSFMSFRYSWLDKLYMVVETLAATI 60
 61 HGAGLPLMMLVFGDMTDTFANAGNIGDGLALL--TNSNNITDTVPYNNLEEDMTRAYAY 117
 61 HGAGLPLMMLVFGDMTDTFANAGNIGDGLALLFNTNTSSNITDTVPYNNLEEDMTRAYAY 120
 118 YSGTAGQVLYAAYIQSPWCLAAQROQIHKKRKFOPTAIRQEIQMFVDYGELENRLTD 177
 121 YSGIGAGVLYAAYIQSPWCLAAQROQIHKKRKFOPTAIRQEIQMFVDYGELENRLTD 180
 181 DVSKINGECDKGMFQSNATFFGFIGFTRGMKLTIVLAIISPVLGSSAAWAKLIS 237
 238 SFTDKELLAYAKAGAVAEYELAATRTVIAGGOKKELERYTKNLBEAKRIGIKKAITANI 297
 241 SFTDKELLAYAKAGAVAEYELAATRTVIAGGOKKELERYTKNLBEAKRIGIKKAITANI 300
 298 SIGAAFLLIYASYALAFWYGTTLVLSKEYSIGVOLTVFSLIGASVGQASPSTEFAPN 357
 301 SIGAAFLLIYASYALAFWYGTTLVLSKEYSIGVOLTVFSLIGASVGQASPSTEFAPN 360
 358 ARGAAFEIKLIDNKESIDSYSKSHPKDNKGUNLFRNVHFSPSREKEVTKLGNLKV 417
 361 ARGAAFEIKLIDNKESIDSYSKSHPKDNKGUNLFRNVHFSPSREKEVTKLGNLKV 420
 418 QSGQTVALVGENSGCCKSITVQLMQRYDTPEGMYSVGDODIRTRNVRFLREIIGVSQEP 477
 421 QSGQTVALVGENSGCCKSITVQLMQRYDTPEGMYSVGDODIRTRNVRFLREIIGVSQEP 480
 478 VLFAATTIAENTRYGRDVDTMDEIEAKYKEANAYDFIMKLQLQKDFTLVGERGAQSGQKQ 537
 481 VLFAATTIAENTRYGRDVDTMDEIEAKYKEANAYDFIMKLQLQKDFTLVGERGAQSGQKQ 540
 538 RIAIALVNRNPKILLDEATSALDDESEAVVQVALIDKARKGRITIVIAHRLSTVRNADV 597
 541 RIAIALVNRNPKILLDEATSALDDESEAVVQVALIDKARKGRITIVIAHRLSTVRNADV 600
 598 IAGFDDGVIVEKGNDBELMEKGKGYFLKVTMOTAGNEIELENAADESKSRDTLEMSSHD 657
 601 IAGFDDGVIVEKGNDBELMEKGKGYFLKVTMOTAGNEIELENAADESKSRDTLEMSSHD 660
 658 SGSSLRKSTRSTRSRTSGSGODRKLSKTEALDESFPVSTWRMKLNNTMPYFVGVFC 717
 661 SGSSLRKSTRSTRSRTSGSGODRKLSKTEALDESFPVSTWRMKLNNTMPYFVGVFC 720
 718 AINGGLQPAFAVISPKLIGIFTRNDDAETKRONSNFLSLFLYVGSITFFLQGFTF 777
 721 AINGGLQPAFAVISPKLIGIFTRNDDAETKRQNSNLFSLFLYVGSITFFLQGFTF 780
 778 GKAGEILTKLRLRYMFRSMRLQDVSDPDKNTGALTRLLANDAQVKAIGSLAIT 837
 781 GKAGEILTKLRLRYMFRSMRLQDVSDPDKNTGALTRLLANDAQVKAIGSLAIT 840
 838 QNIANLGTGIIISLYGWLTLLIAIVPIATAIVSVEMMLSGAOKKELSGAKIA 897
 841 QNIANLGTGIIISLYGWLTLLIAIVPIATAIVSVEMMLSGAOKKELSGAKIA 900
 898 TEATENFRTVSLTQOKFEMYDQSLQPVYRNSLRKAHFGITTSQAMMYSYAGCP 957
 901 TEATENFRTVSLTQOKFEMYDQSLQPVYRNSLRKAHFGITTSQAMMYSYAGCP 960
 958 RFGAYVIAHSLMSFVFLYLYSAVYVGAMAVQVSSAPDYYAKVSAAHIMIETKPL 1017
 961 RFGAYVIAHSLMSFVFLYLYSAVYVGAMAVQVSSAPDAAKVAHIMIETKPL 1020
 1018 IDSYSTEMGLKENTLLEGNTENREVNPYPTRDIPVQSLSEVKGGQTLALVGSSGGKS 1077
 1021 IDSYSTEMGLKENTLLEGNTENREVNPYPTRDIPVQSLSEVKGGQTLALVGSSGGKS 1080
 1078 TVVQILERFYDPLAKVLLDSEKEIKOLNQVWRAHIGIVSOPILFDCSISENTAYDNS 1137

Db Db 1081 TVVQILERFYDPLAKVLLDSEKEIKOLNQVWRAHIGIVSOPILFDCSISENTAYDNS 1140
 Qy Qy 1138 RVSOEETRAKEANTHAFIESLPKISTRVGKGTQLSGGKQRIKARALVYRPHIL 1197
 Db Db 1141 RVSOEETRAKEANTHAFIESLPKISTRVGKGTQLSGGKQRIKARALVYRPHIL 1200
 Qy Qy 1198 LDEATSDALDTESERVQOALDKAREGRCTIVIAHRLSTQNADLIVYFQNGRYKEHGHT 1257
 Db Db 1201 LDEATSDALDTESERVQOALDKAREGRCTIVIAHRLSTQNADLIVYFQNGRYKEHGHT 1260
 Qy Qy 1258 QQLAQKGYPSMYSVQAGKQ 1280
 Db Db 1261 QQLAQKGYPSMYSVQAGKQ 1283

RESULT 6
 US-09-584-586-2
 Sequence 2, Application US/09584586
 Patent No. 6,923,450

GENERAL INFORMATION:

APPLICANT: Sorrentino, Brian
 Bunting, Kevin
 TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 FILE REFERENCE: 1340-1-01CIP
 CURRENT APPLICATION NUMBER: US/09/584,586
 CURRENT FILING DATE: 2000-05-31
 EARLIER APPLICATION NUMBER: US 60/086,988
 EARLIER FILING DATE: 1998-05-28
 EARLIER APPLICATION NUMBER: PCT/US99/11825
 EARLIER FILING DATE: 1999-05-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn Ver.: 2.0
 SEQ ID NO: 2
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Human MDR 185-G
 US-09-584-586-2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MLDLEDGRNGGAEKKFKLANKSKDKKERKPTVSVFSMFRYSWLDKLYMVVETLAII 60
 1 MLDLEDGRNGGAEKKFKLANKSKDKKERKPTVSVFSMFRYSWLDKLYMVVETLAII 60
 61 HGAGLPLMLVFGDMTDFTANAGNUGDLGALLTNNSNITDTPVYMNLERDMTRAYYSG 120
 61 HGAGLPLMLVFGDMTDFTANAGNUGDLGALLTNNSNITDTPVYMNLERDMTRAYYSG 120
 721 IGAGLVAVIYQSVFWCLAGROTICKRKIRQFPHAIMRQEQIGFWPDYHVGELNTRLDDVS 180
 121 IGAGLVAVIYQSVFWCLAGROTICKRKIRQFPHAIMRQEQIGFWPDYHVGELNTRLDDVS 180
 121 IGAGLVAVIYQSVFWCLAGROTICKRKIRQFPHAIMRQEQIGFWPDYHVGELNTRLDDVS 180
 181 KINEGIGDKGFMFQSMATFTGFIVGFTRGWKLTVLIAISPVGLGSAWAKILSSFT 240
 181 KINEGIGDKGFMFQSMATFTGPIVGFTRGWKLTVLIAISPVGLGSAWAKILSSFT 240
 241 DKELLAYAKAGVAAEVLAIRTYIAFGQQKKELEYRNKLEEARIGIKKATANISIG 300
 241 DKELLAYAKAGVAAEVLAIRTYIAFGQQKKELEYRNKLEEARIGIKKATANISIG 300
 301 AAFLIYASALAFWYGTIVLKEYSIGVTTFVSLIGAFSVQGAPSISIAFANARG 360
 301 AAFLIYASALAFWYGTIVLKEYSIGVTTFVSLIGAFSVQGAPSISIAFANARG 360
 361 AAFLIYKIDNKPIDSYSKSGHPDNKGNLLEPRVHESYSPSRKEVILKGJNLKVQSG 420
 361 AAFLIYKIDNKPIDSYSKSGHPDNKGNLLEPRVHESYSPSRKEVILKGJNLKVQSG 420

FILE REFERENCE: 015280-402100US
 CURRENT APPLICATION NUMBER: US 09/767,594
 CURRENT FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: US 60/177,410
 PRIOR FILING DATE: 2000-01-20
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 2
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human P-glycoprotein (Pgp) /multi-drug resistance (ABC transporter) 1
 OTHER INFORMATION: (mdr-1) ATP-binding cassette (ABC transporter)
 OTHER INFORMATION: protein
 US-09-767-594-2

	Query Match	Score	DB 2;	Length
	Best Local Similarity	96.6%	Length	1280;
	Matches 1236;	Conservative 19;	Mismatches 25;	Indels 0;
	Gaps 0;			
Qy	1 MDLEGDRNGGAEEKKNNFKLANKNSKDKKERKPTVSYFSMPRYSNFLDKLYMVVGTLAAII 60			
Db	1 MDLEGDRNGGAEEKKNNFKLANKNSKDKKERKPTVSYFSMPRYSNFLDKLYMVVGTLAAII 60			
Qy	61 HAGAGPLMLMUVGMDTFAANAGQGDGALLTSNSNITDVPNLLEBMTNTYAYYSG 120			
Db	61 HAGAGPLMLMUVGMDTFAANAGQGDGALLTSNSNITDVPNLLEBMTNTYAYYSG 120			
Qy	121 IGAGLVAAATIQVSWICLAGRQTHKIRKOFFHAIIMROEIGFWFDVHGELNTRLTDDVS 180			
Db	121 IGAGLVAAATIQVSWICLAGRQTHKIRKOFFHAIIMROEIGFWFDVHGELNTRLTDDVS 180			
Qy	181 KINECIGDKIGMFPSMATEFTGFVGETGRGMKLTLYVLAISPVLIGLSAAVAKILSSFT 240			
Db	181 KINECIGDKIGMFPSMATEFTGFVGETGRGMKLTLYVLAISPVLIGLSAAVAKILSSFT 240			
Qy	241 DKEILAYAKGVAAEVLLAARIYTAEGQQKKELEBRYNQLEEARIGKIKATTANISIG 300			
Db	241 DKEILAYAKGVAAEVLLAARIYTAEGQQKKELEBRYNQLEEARIGKIKATTANISIG 300			
Qy	301 AAFLIYASALATWYGTIVLVSKEYSICQVLTVFSVSLJIGAFSEVGQAPSIEAFANARG 360			
Db	301 AAFLIYASALATWYGTIVLVSKEYSICQVLTVFSVSLJIGAFSEVGQAPSIEAFANARG 360			
Qy	361 AAFLIYASALATWYGTIVLVSKEYSICQVLTVFSVSLJIGAFSEVGQAPSIEAFANARG 420			
Db	361 AAFLIYASALATWYGTIVLVSKEYSICQVLTVFSVSLJIGAFSEVGQAPSIEAFANARG 420			
Qy	421 OTVALVGNSCGCKSTTVQMLRQDPTEGMSVQGDQIRTINRFLREIGVYSEQPVLF 480			
Db	421 OTVALVGNSCGCKSTTVQMLRQDPTEGMSVQGDQIRTINRFLREIGVYSEQPVLF 480			
Qy	481 ATTIAENIYGREDTMDIEKAVERANAYDFMLPKQFDTLUGERAQLSGCQKQRLA 540			
Db	481 ATTIAENIYGREDTMDIEKAVERANAYDFMLPKQFDTLUGERAQLSGCQKQRLA 540			
Qy	541 TARAIVRNPKILLDEATSALDTESEAVYQVALDKARKRTTIVIAHLSTVNADVTAG 600			
Db	541 TARAIVRNPKILLDEATSALDTESEAVYQVALDKARKRTTIVIAHLSTVNADVTAG 600			
Qy	601 FDDGIVRKGNHDLMKTKGIFYPKLNTQCATNEIELNAADESKSEDTLENSHDSS 660			
Db	601 FDDGIVRKGNHDLMKTKGIFYPKLNTQCATNEIELNAADESKSEDTLENSHDSS 660			
Qy	661 SLLRKRSSTRSVEGQSGQDRLKLSTKEALDESIPPSFRIMKLNTEPYFVGFCAII 720			
Db	661 SLLRKRSSTRSVEGQSGQDRLKLSTKEALDESIPPSFRIMKLNTEPYFVGFCAII 720			
Qy	721 NGGLQPAFAPAFISXIGTFGIVTRNDAAETKRQNSNLISLFLVGLGIVSFITFFLOGFTFGKA 780			
Db	721 NGGLQPAFAPAFISXIGTFGIVTRNDAAETKRQNSNLISLFLVGLGIVSFITFFLOGFTFGKA 780			

RESULT 7
 US-09-767-594-2
 Sequence 2, Application US/0967594
 Patent No. 6521635
 GENERAL INFORMATION:
 APPLICANT: Robey, Robert
 APPLICANT: Bates, Susan
 as represented by the Secretary of the
 Department of Health and Human Services
 APPLICANT: Nggl Qpaafapafisxigtfgivtrndaaetkrqnsnlislf lvglgivsfitfflogftfgka
 APPLICANT: Nggl Qpaafapafisxigtfgivtrndaaetkrqnsnlislf lvglgivsfitfflogftfgka
 TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

Qy	1141	SQEETVRAKEANIHAFIESLPNKYSTKVGDKTGTLGGKQRITARALYRPHILLD	12000
Db	1141	SQEETVRAKEANIHAFIESLPNKYSTKVGDKTGTLGGKQRITARALYRPHILLD	12000
Qy	1201	EATSLDTESEKVVQALDXKAREGRTCIVIAHRLSTIONADLIVFQNSRVKEHGTHOOL	1260
Db	1201	EATSLDTESEKVVQALDXKAREGRTCIVIAHRLSTIONADLIVFQNSRVKEHGTHOOL	1260
Qy	1261	LAQKCIYFSNVSVQAGTKRQ	1280
Db	1261	LAQKCIYFSNVSVQAGTKRQ	1280
RESULT 4			
	US-10-101-433A-5		
	; Sequence 5 , Application US/10101433A		
	; Patent No 6855812		
	; GENERAL INFORMATION		
	; APPLICANT: Hanscom, Sara		
	; APPLICANT: Crespi, Charles		
	; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF		
	; FILE REFERENCE: G00307/20019		
	; CURRENT APPLICATION NUMBER: US/10/101,433A		
	; CURRENT FILING DATE: 2002-03-19		
	; PRIOR APPLICATION NUMBER: US 60/277,095		
	; PRIOR FILING DATE: 2001-03-19		
	; NUMBER OF SEQ ID NOS: 38		
	; SOFTWARE: Patentin version 3.0		
	; SEQ ID NO 5		
	; LENGTH: 1280		
	; TYPE: PRT		
	; ORGANISM: Homo sapiens		
	US-10-101-433A-5		
Query	Match	100.0%	Score 6431; DB 2; Length 1280;
	Best Local Similarity	100.0%	Pred. No. 0;
	Matches 1280; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Dy	1	MDLEGDRNGAKCKNFEKLANKSSEKDKEKPKTVSFNSMFRYSNWLDKLYMVYGTLLAII	60
Db	1	MDLEGDRNGAKCKNFEKLANKSSEKDKEKPKTVSFNSMFRYSNWLDKLYMVYGTLLAII	60
Dy	61	HGAGLPLMLVGFEMTDIFANAGNLIEDLMSNTNSPINDTGFEMNLIEDMTRYAYYSG	120
Db	61	HGAGLPLMLVGFEMTDIFANAGNLIEDLMSNTNSPINDTGFEMNLIEDMTRYAYYSG	120
Dy	121	IGAGVLVAAYIOVSFWCLAAQROIHKRKOFFHAIRQEIWFVDFDVGELNTRITDDVS	180
Db	121	IGAGVLVAAYIQVSFWCLAAQROIHKRKOFFHAIRQEIWFVDFDVGELNTRITDDVS	180
Dy	181	KINEVIGDKGMFFQSMATPTTGFIVGFTRGWKLTLVILLAISPVIGLSAIVWAKILSST	240
Db	181	KINEVIGDKGMFFQSMATPTTGFIVGFTRGWKLTLVILLAISPVIGLSAIVWAKILSST	240
Dy	241	DKELLAYAKAGAAVEVLAIRTVIAFGGOKKELERYNKLNLEEKRIGKKAATANISIG	300
Db	241	DKELLAYAKAGAAVEVLAIRTVIAFGGOKKELERYNKLNLEEKRIGKKAATANISIG	300
Dy	301	AAFLIYASVALATYKTTLVSEBSYSGVLTFFSYLJGAFSVQGSPSTEAFANARG	360
Db	301	AAFLIYASVALAWYGTTLVLSSEBSYSGVLTFFSYLJGAFSVQGSPSTEAFANARG	360
Dy	361	AAYEIFKIDNKNSIDSFSKGKRPDNKIGNLBEFVHFSYSPRSKEVKILKGILNKYQSG	420
Db	361	AAYEIFKIDNKNSIDSFSKGKRPDNKIGNLBEFVHFSYSPRSKEVKILKGILNKYQSG	420
Dy	421	QTVALVGSQGCKGSTTYQLMORLYDPTPEGMVSYDGDQIRTINVRFLIREIIGVVSQEPVLF	480
Db	421	QTVALVGSQGCKGSTTYQLMORLYDPTPEGMVSYDGDQIRTINVRFLIREIIGVVSQEPVLF	480
Dy	481	ATTIAPIVRYGRENVTDIEIKAKEANAYDTMLKPHKFPTLGERRGAGLSGGQKQKRIA	540

Qy	SOEIVRAKEANTHAFTEISLPNKYSTKVGDKTOLSGGOKORIAIAARALVROPHILLID	Db	481 ATTIAENIRYGRENTVMDEIEKAVKANAYDIMEKULPKHFDLTVGERGAOLSGGOKORIA 5400
Db	1141 SOEIVRAKEANTHAFTEISLPNKYSTKVGDKTOLSGGOKORIAIAARALVROPHILLID	Qy	541 IARALVNPKILLDEATSALDTESEAVVOVALDKARKGRITTIVAHLSTVRNADVTAG 600
Qy	1201 EATSLDTESEKVQEALDKAREGRCTCIVIAHRLSTIONADLIVFONGRVEKHGTQL	Db	541 IARALVNPKILLDEATSALDTESEAVVOVALDKARKGRITTIVAHLSTVRNADVTAG 600
Db	1201 EATSLDTESEKVQEALDKAREGRCTCIVIAHRLSTIONADLIVFONGRVEKHGTQL	Qy	601 FDDGTYVEKGHNDELMKEGKJYFLKLYTMOTAGNEYELENADESSEIDALEMSNDRS 660
Qy	1261 LAQKGYFMSVSVQAGTKRQ 1280	Db	601 FDDGTYVEKGHNDELMKEGKJYFLKLYTMOTAGNEYELENADESSEIDALEMSNDRS 660
Db	1261 LAQKGYFMSVSVQAGTKRQ 1280	Qy	661 SLIRKRSPERSURGSQADPKLSTKEALDESIPVSFRWIMKLNTIETWPFLVVGFCII 720
RESULT 4			
	US-10-101-433A-5	Db	661 SLIRKRSPERSURGSQADPKLSTKEALDESIPVSFRWIMKLNTIETWPFLVVGFCII 720
	; Sequence 5 , Application US/10101433A	Qy	721 NGSLQPAFAIFESKIGVTRIDDPETRQNSNLFSLLFLAUGLISSFITFFLGCFTEGKA 780
	; GENERAL INFORMATION:	Db	721 NGSLQPAFAIFESKIGVTRIDDPETRQNSNLFSLLFLAUGLISSFITFFLGCFTEGKA 780
	; APPLICANT: Hanscom, Sara	Qy	781 GBILTKRLRYMVFMSMLRDQYSWDFPNTGALTTRLANDAQVKGAIGSRLIAVITONI 840
	; APPUCIANT: Crespi, Charles	Db	781 GBILTKRLRYMVFMSMLRDQYSWDFPNTGALTTRLANDAQVKGAIGSRLIAVITONI 840
	; TITLE OF INVENTION: -GLICOPROTEINS AND USES THEREOF	Qy	841 ANLGTGIIISPYGMQNTLILIAVPLIAQVWENKMLSGALRKKELEGAKATEA 900
	; FILE REFERENCE: G00307/70019	Db	841 ANLGTGIIISPYGMQNTLILIAVPLIAQVWENKMLSGALRKKELEGAKATEA 900
	; CURRENT APPLICATION NUMBER: US/10/101,433A	Qy	901 IENPFTVVSLSIQEQPERMYAQSLQVPPYRSLRKAHIFGITFSFTQAMMPSYAGCFRFG 960
	; CURRENT FILING DATE: 2002-03-19	Db	901 IENPFTVVSLSIQEQPERMYAQSLQVPPYRSLRKAHIFGITFSFTQAMMPSYAGCFRFG 960
	; PRIOR APPLICATION NUMBER: US 60/277, 095	Qy	961 AYLVAKLMSFEDVLLVSAVFGAMAVGQSSAPDYAKAKISAHIMIETXPLPLIDS 1020
	; PRIOR FILING DATE: 2001-03-19	Db	961 AYLVAKLMSFEDVLLVSAVFGAMAVGQSSAPDYAKAKISAHIMIETXPLPLIDS 1020
	; NUMBER OF SEQ ID NOS: 38	Qy	1021 YSTEGLMPNTLEGNTVFGSUVFNYPTRDIPVGLSLEVVKCGSTV 1080
	; SOFTWARE: PatentIn version 3.0	Db	1021 YSTEGLMPNTLEGNTVFGSUVFNYPTRDIPVGLSLEVVKCGSTV 1080
	; SEQ ID NO: 5	Qy	1081 QLLERFYDPLAGKVLLDKEIKRLNVQWLRHIGTIVSSEPIPDSCTAENIAYGDNSRIVV 1140
	; LENGTH: 1280	Db	1081 QLLERFYDPLAGKVLLDKEIKRLNVQWLRHIGTIVSSEPIPDSCTAENIAYGDNSRIVV 1140
	; TYPE: PRT	Qy	1141 SOEIVRAKEANTHAFTEISLPNKYSTKVGDKTOLSGGOKORIAIAARALVROPHILLID 1200
	; ORGANISM: Homo sapiens	Db	1141 SOEIVRAKEANTHAFTEISLPNKYSTKVGDKTOLSGGOKORIAIAARALVROPHILLID 1200
Qy	US-10-101-433A-5	Qy	1201 BATSALDTESEKVKQELDKAEGRTCTIVIAHRLSTQNADLIVFONGRVEKHGTQL 1260
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 MDLEGDRNGGAKKKNNPFKLANKSEKDKGCKRPTVSYSMFPRYSNWLDKLYMVVGTLAAII	Db	1201 BATSALDTESEKVKQELDKAEGRTCTIVIAHRLSTQNADLIVFONGRVEKHGTQL 1260
	1 MDLEGDRNGGAKKKNNPFKLANKSEKDKGCKRPTVSYSMFPRYSNWLDKLYMVVGTLAAII	Qy	1261 LAQKGYFMSVSVQAGTKRQ 1280
	61 HAGCLPLMMLYFGMTDIPANGNLEDLMSNITNRSINTDGFPMNLLEDMTRYAYYYSG	Db	1261 LAQKGYFMSVSVQAGTKRQ 1280
	61 HAGCLPLMMLYFGMTDIPANGNLEDLMSNITNRSINTDGFPMNLLEDMTRYAYYYSG	Qy	1261 LAQKGYFMSVSVQAGTKRQ 1280
Dy	121 IGGGVLYAIIYQSFWLCLAQRGTHKIRKOFFHAIMRQGTFTRGWLTLVILASPYVLGLSAAWAKILSSPT	Db	1261 LAQKGYFMSVSVQAGTKRQ 1280
Db	121 IGGGVLYAIIYQSFWLCLAQRGTHKIRKOFFHAIMRQGTFTRGWLTLVILASPYVLGLSAAWAKILSSPT	Qy	1280
Dy	181 KINEVGDKIGHMFQSMATEPTGFIQVTRGWLTLVILASPYVLGLSAAWAKILSSPT	Db	1280
Db	181 KINEVGDKIGHMFQSMATEPTGFIQVTRGWLTLVILASPYVLGLSAAWAKILSSPT	Qy	240
b	181 KINEVGDKIGHMFQSMATEPTGFIQVTRGWLTLVILASPYVLGLSAAWAKILSSPT	Db	240

RESULT 5
US-09-817-762-3
Sequence 3, Application US/09817762
Patent No. 6858724

; GENERAL INFORMATION:

; APPLICANT: Spalding, Edgar P.
; ADDRESS: 1000 N. University,
; CITY: Bos₁
; STATE: MA
; ZIP: 02135
; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 DATABASE ACCESION NUMBER: Genbank P00183
 DATABASE ENTRY DATE: 1997-11-01
 US-09-817-162-3

Query Match 100.0%; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLEGDNGGAKKNNFKLNNKSEDKKEKCPVSVSMFRYSNWLDLYMVGTLLAII 60
 Db 1 MDLEGDNGGAKKNNFKLNNKSEDKKEKCPVSVSMFRYSNWLDLYMVGTLLAII 60

Qy 61 HAGALPMLMVFGEMTDFANAGNLEDMSNTNSDINDTGFEMMLEDMTRYAYYSG 120
 Db 61 HAGALPMLMVFGEMTDFANAGNLEDMSNTNSDINDTGFEMMLEDMTRYAYYSG 120

Qy 121 IGGAVLVAYIYQSFWCLAAQGQHKKRKOFPHTAIMQEIGFEDVGDVNGEATRLDDVS 180
 Db 121 IGGAVLVAYIYQSFWCLAAQGQHKKRKOFPHTAIMQEIGFEDVGDVNGEATRLDDVS 180

Qy 181 KINEVIGDKIGRFQSNATFFGPIVCFTRGMPLTLVILAIASPVLGSAAWAKILSFT 240
 Db 181 KINEVIGDKIGRFQSNATFFGPIVCFTRGMPLTLVILAIASPVLGSAAWAKILSFT 240

Qy 241 DKELLAYAKAGAAEETVLAIAITVIAFGQKBLERVNKOLEBARKIGKKAITANISIG 300
 Db 241 DKELLAYAKAGAAEETVLAIAITVIAFGQKBLERVNKOLEBARKIGKKAITANISIG 300

Qy 301 AAFLIYASYALAFMVTIUSGEYSIGQUTVPESVLIGASVGCONSPLEAFNARG 360
 Db 301 AAFLIYASYALAFMVTIUSGEYSIGQVLTIVSGEYSIGQVLTIVSGEYSIGQVLTIVSG 360

Qy 361 AAYEIKIIDKPKSIISYSKSCHKPDNIKGNLFRNVHSYPSRSKREVKLIGLNLYKVQSG 420
 Db 361 AAYEIKIIDKPKSIISYSKSCHKPDNIKGNLFRNVHSYPSRSKREVKLIGLNLYKVQSG 420

Qy 421 QTVALVGNISGCCKSTTVQLMORLYDPFGMYSVGDQDRTINVRFLREITCVSOPVLF 480
 Db 421 QTVALVGNISGCCKSTTVQLMORLYDPFGMYSVGDQDRTINVRFLREITCVSOPVLF 480

Qy 481 ATTIAINRYGRENNTMDEIEKAVKEANAYDFIMKLPHKEDTLVGERGAOLSGGQKQRIA 540
 Db 481 ATTIAINRYGRENNTMDEIEKAVKEANAYDFIMKLPHKEDTLVGERGAOLSGGQKQRIA 540

Qy 541 IARALVNPKILLDEATSLDTESEAVQVALDKARKGRITVIARHLSVTRNDVIAG 600
 Db 541 IARALVNPKILLDEATSLDTESEAVQVALDKARKGRITVIARHLSVTRNDVIAG 600

Qy 601 FDDGVIVKEGNHDLMKEKGIFYKLVMTMOTAGNEVELENNADESKEBDIALEMSSNDRS 660
 Db 601 FDDGVIVKEGNHDLMKEKGIFYKLVMTMOTAGNEVELENNADESKEBDIALEMSSNDRS 660

Qy 661 SLIRKRSTRRSYRGSOAQDRKLSTKEBALDESIPSYFWRIMKLUNITEWPFVGHPCAI 720
 Db 661 SLIRKRSTRRSYRGSOAQDRKLSTKEBALDESIPSYFWRIMKLUNITEWPFVGHPCAI 720

Qy 721 NGGLQPAFAIFPSKIGFRRIDDPETKRSNLSLLFLALGIISFITPLQGPTFGKA 780
 Db 721 NGGLQPAFAIFPSKIGFRRIDDPETKRSNLSLLFLALGIISFITPLQGPTFGKA 780

Qy 781 GEILTYKLRMVMFRSMLRQDVSWFDDPKNTGALTRLANDAQQVKGAGSRSLAVTONI 840
 Db 781 GEILTYKLRMVMFRSMLRQDVSWFDDPKNTGALTRLANDAQQVKGAGSRSLAVTONI 840

Qy 841 AN4GTSLLISFLYGNQLTLLIATIYVIAIAGVYVEMKMSQALDKKUELEGAKIATEA 900
 Db 841 AN4GTSLLISFLYGNQLTLLIATIYVIAIAGVYVEMKMSQALDKKUELEGAKIATEA 900

Qy 901 IENFRTVSLSLTQEQKFBHYAOSLOVPRYNSLRKAIIQTTFSFTQAMMFTSYAGGCRFG 960
 Db 901 IENFRTVSLSLTQEQKFBHYAOSLOVPRYNSLRKAIIQTTFSFTQAMMFTSYAGGCRFG 960

Qy 961 AYLVAHKLMSFEDVLLVFSAVFGAMAVGOVSSPAPDYAKAKISAHIMMITKEPLIDS 1020
 Db 961 AYLVAHKLMSFEDVLLVFSAVFGAMAVGOVSSPAPDYAKAKISAHIMMITKEPLIDS 1020

Qy 1021 YSTEGLMPNTLEGNTTGEVYENYPTRDPIVLOGLSLEVKGOTALVGSGCCSKSTVV 1080
 Db 1021 YSTEGLMPNTLEGNTTGEVYENYPTRDPIVLOGLSLEVKGOTALVGSGCCSKSTVV 1080

Qy 1081 QLERFTDPLAKVLLDGEKTKRANVOWLAHIGVSQEPPLPDSIAENIAYGNSRVV 1140
 Db 1081 QLERFTDPLAKVLLDGEKTKRANVOWLAHIGVSQEPPLPDSIAENIAYGNSRVV 1140

Qy 1141 SOEETVRAAKEANIAHIESLPNKYSTKVDKGTOQVLSGGOKORIALARALYRPHILLLD 1200
 Db 1141 SOEETVRAAKEANIAHIESLPNKYSTKVDKGTOQVLSGGOKORIALARALYRPHILLLD 1200

Qy 1201 EATSLADTESEKVKVQDAELDKAREGTCIVTAHRLSTIONADLIVYFQNGRKYKEHSTHQL 1260
 Db 1201 EATSLADTESEKVKVQDAELDKAREGTCIVTAHRLSTIONADLIVYFQNGRKYKEHSTHQL 1260

Qy 1261 LAQKGYFMSWVSVQAGTKRQ 1280
 Db 1261 LAQKGYFMSWVSVQAGTKRQ 1280

RESULT 6
 US-09-584-586-4
 Sequence 4, Application US/09584586
 Percent No. 633150

GENERAL INFORMATION:
 / APPLICANT: Sorrentino, Brian
 / APPLICANT: Bunting, Kevin
 / TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 / TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 / FILE REFERENCE: 1340-1-021CIP
 / CURRENT APPLICATION NUMBER: US/09/584,586
 / CURRENT FILING DATE: 2000-05-31
 / EARLIER APPLICATION NUMBER: US 60/086,988
 / EARLIER FILING DATE: 1998-05-28
 / EARLIER APPLICATION NUMBER: PCT/US99/11825
 / EARLIER FILING DATE: 1999-05-27
 / NUMBER OF SEQ ID NOS: 16
 / SOFTWARE: Patentin ver. 2.0
 / SEQ ID NO 4
 / LENGTH: 1280
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: Human MDR 185-V
 US-09-584-586-4

Query Match 100.0%; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0; Mis matches 0; Indels 0; Gaps 0;

Matches 1280; Conservative 0; Mis matches 0; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGGAKKNNFKLNNKSEKDKEKKKPTVSVSMFRYSNWLDLYMVGSTLAII 60
 Db 1 MDLEGDRNGGAKKNNFKLNNKSEKDKEKKKPTVSVSMFRYSNWLDLYMVGSTLAII 60

Qy 61 HGAGIPLMMLVGETMDIFPANGNELEDMSNTNRSNDTGFPMNLBEDMTYAYYSG 120
 Db 61 HGAGIPLMMLVGETMDIFPANGNELEDMSNTNRSNDTGFPMNLBEDMTYAYYSG 120

Qy 121 IGAGVLYAAIYQSFWCLLAGRQHKKRQFFIAIMROIGFWDHYGELNLTRTDIVS 180
 Db 121 IGAGVLYAAIYQSFWCLLAGRQHKKRQFFIAIMROIGFWDHYGELNLTRTDIVS 180

Qy 181 KINEVIGDKIGMFQSMATFTGTFITGTRGWKLTLVILAIISPVLGISAAYWAKILSSFT 240

181 KINEVIGDKIGMFQSMATFFGPIVGFRGKRLTVLIALSPVLGLSAAWAKILSSFT 240
 QY 241 DKELLAYAKAGAVAEEVTAATRTVIAFGQKBLERYNKNEEAKIGKKAITANISIG 300
 Db 241 DKELLAYAKAGAVAEEVLAATRTVIAFGQKBLERYNKNEEAKIGKKAITANISIG 300
 ; RESULT 7
 ; US-08-583-276-19
 ; Sequence 19 ; Application US/08583276
 ; Patent No. 5937516
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonagh, Kevin T.
 ; Inventor: McDonagh, Kevin T.
 ; APPLICANT: Nierhaus, Arthur
 ; Inventor: Nierhaus, Arthur
 ; APPLICANT: Tolstoshev, Paul
 ; Inventor: Tolstoshev, Paul
 ; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
 ; MULTIDRUG RESISTANCE GENES AND IMPROVED
 ; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
 ; ADDRESS: Cecchi & Stewart
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: DNA V2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/583,276
 ; FILING DATE: 05-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/332,444
 ; FILING DATE: 31-OCT-1994
 ; APPLICATION NUMBER: 07/887,712
 ; FILING DATE: 22-MAY-1992
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1280 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; PROTEIN
 ; US-08-583-276-19

Query Match 99.9%; Score 6428; DB 1; Length 1280;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGDRNGGAKKKNNKFPLNNKSEKDKEKEKETVSYFSMPRYSNWLDKLYNNVGTLLAII 60
 Db 1 MDJEGDRNGGAKKKNNKFPLNNKSEKDKEKEKETVSYFSMPRYSNWLDKLYNNVGTLLAII 60
 QY 61 HGAGPLIMMLVFGEMTDIFANGNLNEDMSNTNRSDINDGFVNMLEEDTRAYYYSG 120
 Db 61 HGAGPLIMMLVFGEMTDIFANGNLNEDMSNTNRSDINDGFVNMLEEDTRAYYYSG 120
 QY 721 NGGLQAFALPSKIGVTRIDDPETKRONSNLSSLFLALGIIISITPFLQGFTFGA 780
 Db 721 NGGLQAFALPSKIGVTRIDDPETKRONSNLSSLFLALGIIISITPFLQGFTFGA 780
 QY 781 GEILTKRLRMYMFRSMRQDODPKNITGALTLLANDAAQVKGAIGSRSLAVITONI 840
 Db 781 GEILTKRLRMYMFRSMRQDODPKNITGALTLLANDAAQVKGAIGSRSLAVITONI 840
 QY 841 ANLGTGIIISIPIYGWQLTLLALATPVIIATGVEMKMSQALKDKELEGACKIATEA 900
 Db 841 ANLGTGIIISIPIYGWQLTLLALATPVIIATGVEMKMSQALKDKELEGACKIATEA 900
 QY 901 TENPTVVSLTQEKFEMYAQSLOVPTNSLRKAHIGTTSFQAMMYSFAGCFREG 960
 Db 901 TENPTVVSLTQEKFEMYAQSLOVPTNSLRKAHIGTTSFQAMMYSFAGCFREG 960
 QY 961 AYLVAHKLMSFEDVLLVFAVVFAMAAGVQYSSPAPDYZAKAKISAHIMIIEKTPLIDS 1020
 Db 961 AYLVAHKLMSFEDVLLVFAVVFAMAAGVQYSSPAPDYZAKAKISAHIMIIEKTPLIDS 1020
 QY 1022 YSTGGLMPTLEGNVTFGEVVFENYTPRDPVYQGLSLFEVKGKOTLAVGSSGGKSTV 1080
 Db 1022 YSTGGLMPTLEGNVTFGEVVFENYTPRDPVYQGLSLFEVKGKOTLAVGSSGGKSTV 1080
 QY 1081 QLERFYDPLAKVLLDGEIKRNLVQTMRAHICLIVSQSPLFDCSIAGNDSRV 1140
 Db 1081 QLERFYDPLAKVLLDGEIKRNLVQTMRAHICLIVSQSPLFDCSIAGNDSRV 1140
 QY 1141 SQEEIVRAKEANHTAIFISSLPNKYKSTVGDKGTLQSGQKQRIATAALVRPHILLID 1200
 Db 1141 SQEEIVRAKEANHTAIFISSLPNKYKSTVGDKGTLQSGQKQRIATAALVRPHILLID 1200
 QY 1201 EATSALDTSEKTYQEALDKEAREGRTCTVIAHRLSTICTIONADLTVFONGRVEKHGTHQOL 1260
 Db 1201 EATSALDTSEKTYQEALDKEAREGRTCTVIAHRLSTICTIONADLTVFONGRVEKHGTHQOL 1260
 QY 1261 LAQKGIYPSMVSVOAGTKRQ 1280
 Db 1261 LAQKGIYPSMVSVOAGTKRQ 1280
 QY 301 AAFLLIYASIALAFWYGTTLVLSGENSIGQVLTVPFSLIGAFSVQASPIEAFANARG 360
 Db 301 AAFLLIYASIALAFWYGTTLVLSGENSIGQVLTVPFSLIGAFSVQASPIEAFANARG 360

Db	418	QSGQTVALVGNSGGCKSSTVQLMQLYDPTBGMVSVDGDIRTINVRFLREIIGVYSEQP	477
Qy	481	VLFATTAAENTRYGREPTVMDTEIEKAVKEANAYDFIMKLPOKFDTLVGERGAQLSGGQQ	540
Db	478	VLFATTAAENTRYGREPTVMDTEIEKAVKEANAYDFIMKLPOKFDTLVGERGAQLSGGQQ	537
Qy	541	RIAIAALPVNPKILLDEATSALDTESEAUVQVALDKARGRTTIVIAHRLSTVNADV	600
Db	538	RIAIAALPVNPKILLDEATSALDTESEAUVQVALDKARGRTTIVIAHRLSTVNADV	597
Qy	601	IAGFDGVIVEKGNADELMRKKGIVYFKLVTNTAGNEIELENADESKSEIDTLEMSHD	660
Db	598	IAGFDGVIVEKGNADELMRKKGIVYFKLVTNTAGNEIELENADESKSEIDTLEMSHD	657
Qy	661	SGSSLIRKRSTRSRVRSQGODRKLSTKEALDESIPPSFWRIMCLNLTEMVYFVGVFC	720
Db	658	SGSSLIRKRSTRSRVRSQGODRKLSTKEALDESIPPSFWRIMCLNLTEMVYFVGVFC	717
Qy	721	AINGGQPAFAVFSKIGIFTRNDAAETDKRQNSHISFLSLFLVGTVSFTFFLOGFTF	780
Db	718	AINGGQPAFAVFSKIGIFTRNDAAETDKRQNSHISFLSLFLVGTVSFTFFLOGFTF	777
Qy	781	GKAGETITKRLRMYFVRSRMRQDVSNFDDPNTTGALLTRLANDAQVKGAIGSRLAIIIT	840
Db	778	GKAGETITKRLRMYFVRSRMRQDVSNFDDPNTTGALLTRLANDAQVKGAIGSRLAIIIT	837
Qy	841	QNTANTGIGLISLIVQWQLTLLLAIVPLIAAGTVEMKNLSQAQLDKKELEGAKGKIA	900
Db	838	QNTANTGIGLISLIVQWQLTLLLAIVPLIAAGTVEMKNLSQAQLDKKELEGAKGKIA	897
Qy	901	TEAIENFRTVLTVSLTQEOKFERNYDQSQVPTNSLRKAHITGITSFTQAMMFYSTAGCF	960
Db	898	TEAIENFRTVLTVSLTQEOKFERNYDQSQVPTNSLRKAHITGITSFTQAMMFYSTAGCF	957
Qy	961	RGAYLVAHSLMSFEDVLVLSAVVFGAMAQGVSSAPDYAKAVYSAAHIMILEKTPL	1020
Db	958	RGAYLVAHSLMSFEDVLVLSAVVFGAMAQGVSSAPDYAKAVYSAAHIMILEKTPL	1017
Qy	1021	IDSYSTGLKENTLEGNTVNEVFNYPTRLDIPVQGLSLEVKKQGTLALVGSSCGKS	1080
Db	1018	IDSYSTGLKENTLEGNTVNEVFNYPTRLDIPVQGLSLEVKKQGTLALVGSSCGKS	1077
Qy	1081	TVVQVLIERFYDPLAKVLLDGEBIKIQKVNQVTRHLIGIVSOPILFCISSENIAYGDSN	1140
Db	1078	TVVQVLIERFYDPLAKVLLDGEBIKIQKVNQVTRHLIGIVSOPILFCISSENIAYGDSN	1137
Qy	1141	RVVSQEPIVRAKEANHTAFIESLPNKYSTRYVGDKGQTLSGGQKORIAIAHALVROPHIL	1200
Db	1138	RVVSQEPIVRAKEANHTAFIESLPNKYSTRYVGDKGQTLSGGQKORIAIAHALVROPHIL	1197
Qy	1201	LIDDEATSLADTESEKVVYQEALDKAREGRTCTIVIAHRLSTQNADLIVFQNGRVKEGTH	1260
Db	1198	LIDDEATSLADTESEKVVYQEALDKAREGRTCTIVIAHRLSTQNADLIVFQNGRVKEGTH	1257
Qy	1261	QOLLAQKGIYPSMVSYOAGAKQ	1283
Db	1258	QOLLAQKGIYPSMVSYOAGAKQ	1280
RESULT 5			
AC	MDR1_HUMAN	STANDARD,	PRT; 1280 AA.
AC	P08133;	Q12755; QL4872;	
DT	01-NOV-1998,	Integrated into UniProtKB/Swiss-Prot.	
DT	01-NOV-1997,	sequence version 2.	
DT	07-MAR-2006,	entry version 78.	
DE	Multi-drug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).		
GN	Name=ABC1; Synonyms=MDR1; PGY1;		
OS	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buaerontoglires; Primates; Catarrhini; Hominoidea;		
OC	Homo.		
NCBI_TaxID	9=606;		

- [1] NUCLEOTIDE SEQUENCE [mRNA], AND VARIANT VAL-185
RN RP MEDLINE=87028230; PubMed=2876781; DOI=10.1016/0092-8674(86)90595-7;
RX RA Chen C.-J., Chin J.-E., Ueda K., Clark D.P., Pastan I., Gottesman M.M.,
RA Roninson I.B.; "Internal duplication and homology with bacterial transport proteins
RT in the mdr1 (P-glycoprotein) gene from multidrug-resistant human
RT cells"; Cell 47:381-389 (1986).
RL RN [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP RX MEDLINE=9009448; PubMed=1967175;
RX RA Chen C.-J., Clark D.P., Ueda K., Pastan I., Gottesman M.M.,
RA Roninson I.B.; "Genomic organization of the human multidrug resistance (MDR1) gene
RT and origin of P-glycoproteins"; J. Biol. Chem. 265:506-514 (1990).
RN [3]
RN NUCLEOTIDE SEQUENCE [mRNA], AND VARIANT VAL-185.
RP RX MEDLINE=97190336; PubMed=9039218; DOI=10.1074/jbc.272.9.5413;
RX RA Chen G., Duran G.B., Steiger K.A., Lacayo N.J., Jaffrezou J.P.,
RA Dumontet C., Sikic B.I.; "Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein,
RT altered phenotype, and resistance to cyclosporins."; J. Biol. Chem. 272:5974-5982 (1997).
RN [4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LEU-17, ASP-21;
RP RX MEDLINE=LYS-566; CYS-593; VAL-1018; ALA-1051; THR-1141 AND ILE-1251;
RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
RA Swanson J.E., McFarland I., Yool B., Park C., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES156718, Department
RT of Genome Sciences, Seattle, WA (URL: http://esp.niehs.nih.gov);
RT Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
RN [5]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP RX MEDLINE=22737939; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McBerthon C., Layman C., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.B.,
RA Fawell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isaak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalichi J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Koziolowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stroymatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marrs M.A., Raymond C., Haugen E.,
RA Gilbert W., Zhou Y., James R., Phelps K., Iordanoff S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.E., Keibler E., Flicek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chiwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green B.D.,
RA Waterston R.H., Wilson R.K.; "The DNA sequence of human chromosome 7.";
RN RT Nature 424:157-164 (2003).
RN [6]
RN NUCLEOTIDE SEQUENCE OF 178-215 AND 800-856.
RP RX MEDLINE=9029529; PubMed=1972623;
RA GEKELER V., WEGER S., PROBST H.; "mdr1/P-glycoprotein gene segments analyzed from various human
RT leukemic cell lines exhibiting different multidrug resistance
RT profiles"; Biochem. Biophys. Res. Commun. 169:796-802 (1990).
RN [7]
RN NUCLEOTIDE SEQUENCE OF 1-23, AND VARIANT SER-893.
RP RX MEDLINE=89312246; PubMed=2568832;
RA Kioka N., Tsutobata J., Kakehi Y., Komano T., Gottesman M.M., Pastan I.,
Ueda K.;

PT	"P-glycoprotein gene (MDR1) cDNA from human adrenal: normal P-glycoprotein carries Gly185 with an altered pattern of multidrug resistance"; Biochem. Biophys. Res. Commun. 162:224-231(1989); [8].	RX	Medline=211686803; PubMed=11829140; DOI=10.1007/s10038-002-8653-6;
RT	RA Saito S., Tida A., Sekine A., Miura Y., Ogawa C., Kawachi S., Higuchi S., Nakamura Y.	RA	Saito S., Tida A., Sekine A., Miura Y., Ogawa C., Kawachi S., Higuchi S., Nakamura Y.
RL	"Three hundred twenty-six genetic variations in genes encoding nine members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the Japanese population." J. Hum. Genet. 47:38-50 (2002).	RT	"Three hundred twenty-six genetic variations in genes encoding nine members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the Japanese population." J. Hum. Genet. 47:38-50 (2002).
RN	REVIEW.	RT	FUNCTION: Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells.
RP	Kerb R., Hoffmeyer S., Brinkmann U.; "ABC drug transporters: hereditary polymorphisms and pharmacological impact in MDR1, MRP1 and MRP2." Pharmacogenomics 2:51-64 (2001); [9].	RT	SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
RN	VARIANT VAL-185; PubMed=11258197; DOI=10.1517/14622416.2.1.51;	RT	TISSUE SPECIFICITY: Expressed in liver, kidney, small intestine and brain.
RP	RNA	CC	POLYMORPHISM: Genetic variation in ABCB1 may play a role in patients who do not respond to drug treatment.
RN	Kerb R., Hoffmeyer S., Brinkmann U.; "An altered pattern of cross-resistance in multidrug-resistant human cells results from spontaneous mutations in the mdr1 (P-glycoprotein) gene." Cell 52:519-529 (1998).	CC	CC
RN	VARIANT SER-893 AND THR-990; MEDLINE=88223345; PubMed=2897240;	CC	SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
RP	RNA	CC	SIMILARITY: Contains 2 ABC transmembrane type-1 domains.
RN	Mickley L.A., Lee J.-S., Weng Z., Alvarez M., Wilson W., Bates S.E., Pojo T.; "Genetic polymorphism in MDR-1: a tool for examining allelic expression in normal cells, unselected and drug-selected cell lines, and human tumors." Blood 91:1749-1756 (1998).	CC	SIMILARITY: Contains 2 ABC transporter domains.
RN	[10]	CC	CAUTION: Ref. 5 (AAB69423) sequence differs from that shown due to erroneous gene model prediction.
RN	VARIANT ASP-21.	CC	DATABASE: NMDB=Atlas Genet. Cytoogenet. Oncol. Haematol. www="http://www.infobiogen.fr/services/chromancer/Genes/PGY1D105.html".
RX	Medline=98139471; PubMed=9473242;	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms distributed under the Creative Commons Attribution-NoDerivs License
RA	Mickley L.A., Lee J.-S., Weng Z., Alvarez M., Wilson W., Bates S.E., Pojo T.; "Genetic polymorphism in MDR-1: a tool for examining allelic expression in normal cells, unselected and drug-selected cell lines, and human tumors." Blood 91:1749-1756 (1998).	CC	DR EMBL: M14758; AAAS9575.1; mRNA.
RA	Medline=202513368; PubMed=10790226;	CC	DR EMBL: M29424; AAAS9576.1; Genomic DNA.
RA	DOI=10.1002/(SICI)1098-1004(200005)15:5<486::AID-HUMU26>3.3.CO;2-G;	CC	DR EMBL: M29425; AAAS9576.1; JOINED; Genomic DNA.
RA	DeeLeves X., Chevillard S., Charpentier C., Vielh P., Laplanche J.L.; "A new polymorphism (N21D) in the exon 2 of the human MDR1 gene encoding the P-glycoprotein"; Hum. Mutat. 15:485-486 (2000).	CC	DR EMBL: M29426; AAAS9576.1; JOINED; Genomic DNA.
RA	Medline=10204660; PubMed=1016719; DOI=10.1073/pnas.050585397;	CC	DR EMBL: M29427; AAAS9576.1; JOINED; Genomic DNA.
RA	Hoffmeyer S., Burk O., von Richter O., Arnold H.P., Brockmeier J.J., John A., Cascorbi I., Gerloff T., Roots I., Eichelbaum M., Brinkmann U.; "Functional polymorphisms of the human multidrug-resistance gene: multiple sequence variations and correlation of one allele with P-glycoprotein expression and activity in vivo." Proc. Natl. Acad. Sci. U.S.A. 97:3473-3478 (2000).	CC	DR EMBL: M29428; AAAS9576.1; JOINED; Genomic DNA.
RA	VARIANT ASP-21; ASN-400; LEU-103 AND ASN-400.	CC	DR EMBL: M29429; AAAS9576.1; JOINED; Genomic DNA.
RA	Medline=10204660; PubMed=1016719; DOI=10.1073/pnas.050585397;	CC	DR EMBL: M29430; AAAS9576.1; JOINED; Genomic DNA.
RA	Hoffmeyer S., Burk O., von Richter O., Arnold H.P., Brockmeier J.J., John A., Cascorbi I., Gerloff T., Roots I., Eichelbaum M., Brinkmann U.; "Functional polymorphisms of the human multidrug-resistance gene: multiple sequence variations and correlation of one allele with P-glycoprotein expression and activity in vivo." Proc. Natl. Acad. Sci. U.S.A. 97:3473-3478 (2000).	CC	DR EMBL: M29431; AAAS9576.1; JOINED; Genomic DNA.
RA	VARIANT ASP-21; ASN-400; SER-893 AND PRO-1107.	CC	DR EMBL: M29432; AAAS9576.1; JOINED; Genomic DNA.
RA	Medline=21135363; PubMed=11240981; DOI=10.1067/mcp.2001.114164;	CC	DR EMBL: M29433; AAAS9576.1; JOINED; Genomic DNA.
RA	Cascorbi I., Gerloff T., John A., Meissel C., Hoffmeyer S., Schwab M., Schaeffeler E., Eichelbaum M., Brinkmann U., Roots I.; "Frequency of single nucleotide polymorphisms in the P-glycoprotein drug transporter MDR1 gene in white subjects." Clin. Pharmacol. Ther. 69:169-174 (2001).	CC	DR EMBL: M29434; AAAS9576.1; JOINED; Genomic DNA.
RA	VARIANT LYS-108.	CC	DR EMBL: M29435; AAAS9576.1; JOINED; Genomic DNA.
RP	PubMed=15618700; DOI=10.2133/dmpk.17.479;	CC	DR EMBL: M29436; AAAS9576.1; JOINED; Genomic DNA.
RA	Honda T., Dan Y., Koyabu N., Ieiri I., Otsubo K., Higuchi S., Ohtani H., Sawada J.; "Polymorphism of MDR1 gene in healthy Japanese subjects: a novel SNP with an amino acid substitution (Glu188Lys)." Drug Metab. Pharmacokinet. 17:479-481 (2002).	CC	DR EMBL: M29437; AAAS9576.1; JOINED; Genomic DNA.
RA	VARIANT ILE-1251.	CC	DR EMBL: M29438; AAAS9576.1; JOINED; Genomic DNA.
RP	PubMed=15618713; DOI=10.2133/dmpk.17.566;	CC	DR EMBL: M29439; AAAS9576.1; JOINED; Genomic DNA.
RA	Ieda M., Saito Y., Konamura K., Ueno K., Kamakura S., Ozawa S., Sawada J.; "Twelve novel single nucleotide polymorphisms in ABCB1/MDR1 among Japanese patients with ventricular tachycardia who were administered amiodarone." Drug Metab. Pharmacokinet. 17:566-571 (2002).	CC	DR EMBL: M29440; AAAS9576.1; JOINED; Genomic DNA.
RA	VARIANT SER-893 AND THR-893.	CC	DR EMBL: M29441; AAAS9576.1; JOINED; Genomic DNA.

Qy	1 MDLEGDRNGGAEKKNFPLNNKSICDKCERKEPTVSMSMFRYSNWLDLXNYVGTLLAAI	60	Db	1078 TTVQOLLERFYDPLAKVLLDGKEIKQLNQVWLRAHGLIVSQEPITFDCTS1SENIAYGDNS	1137	
Db	1 MDLEGDRNGGAKKNFPLNNKSICDKCERKEPTVSMSMFRYSNWLDLXNYVGTLLAAI	60	Qy	1141 RVVSQEETIPRAAKENIHAFTELESNKYSYTRVGDKTOLSGGOKRRIARALYTRPHFI	1200	
Qy	61 HAGAIPMLMVFQDMTDIFANAGNLGDIGALLFNNNTNSNITDTVPMLNLEDMTRYAYY	120	Db	1138 RVVSQEETIPRAAKENIHAFTELESNKYSYTRVGDKTOLSGGOKRRIARALYTRPHFI	1197	
Db	61 HAGAIPMLMVFQDMTDIFANAGNLGDIGALL--TNSNITDTVPMLNLEDMTRYAYY	117	Qy	1201 LDDEATSALDTESETRVQRLDKAREGTCIVIARLSTQNADLIVVONGRYKEHGHT	1260	
Qy	121 YSGIGACVLUAXIOUSPFWCLLAAGRQTHKIRKOPFHAIIMPROTGWDFHDGELNTRLTD	180	Db	1198 LDDEATSALDTESETRVQRLDKAREGTCIVIARLSTQNADLIVVONGRYKEHGHT	1257	
Db	118 YSGIGACVLUAXIOVSFWCLLAAGRQTHKIRKOPFHAIIMPROTGWDFHDGELNTRLTD	177	Qy	1261 QOLLQAGIYFSMVSQVAGKQ 1283		
Qy	181 DVSKINGIGDKLGMPPQSMAFPFTGTVGPFPGMLTLVLLIASPVTGSLSAVWAKLS	240	Db	1258 QOLLQAGIYFSMVSQVAGKQ 1280		
Db	178 DVSKINGIGBKGMPPQSMAFPFTGTVGPFPGMLTLVLLIASPVLGSLSAVWAKLS	237	RESULT 6 US-09-584-586-2 ; Sequence 2, Application US/09584586 ; Patent No. 6933150.			
Qy	241 SFTDKELLAYAKAGVAEVLAILRTAAGQSKKLERYKNLEARKRIGKALTANI	300	GENERAL INFORMATION:			
Db	238 SFTDKELLAYAKAGVAEVLAILRTAAGQSKKLERYKNLEARKRIGKALTANI	297	APPLICANT: Sorrentino, Brian			
Qy	301 SIGAAPLIIYASVALAFTWGTGTTVLSKEYSTGQVJTFVSFLGAFSVGOASPSTBAPAN	360	APPLICANT: Bunting, Kevin			
Db	298 SIGAAPLIIYASVALAFTWGTGTTVLSKEYSTGQVJTFVSFLGAFSVGOASPSTBAPAN	357	TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH			
Qy	361 ARGAAPFIFC1DNKESIDSYSKSCKHPDN1GNLNEPRNTNFSYPSRSKEVTKLGNLKV	420	TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF			
Db	358 ARGAAPFIFC1DNKPSDTSYSKSCKHPDN1GNLNEPRNTNFSYPSRSKEVTKLGNLKV	417	FILE REFERENCE: 1340-1-021CIP			
Qy	421 QSGQTVALGVNSGCCGKSTTQLMQRLYDTPTEGMVSYDQDIRTINVRFLRELTGIVSQEP	480	CURRENT FILING DATE: 2000-05-31			
Db	418 QSGQTVALGVNSGCCGKSTTQLMQRLYDTPTEGMVSYDQDIRTINVRFLRELTGIVSQEP	477	EARLIER APPLICATION NUMBER: US 60/086,988			
Qy	481 VLFATTIAENTTRYGREDTMDLEKAVKEAYANAYDFIMKLPOKFDTLVGERQSLGQQQ	540	EARLIER FILING DATE: 1998-05-28			
Db	478 VLFATTIAENTTRYGREDTMDLEKAVKEAYANAYDFIMKLPOKFDTLVGERQSLGQQQ	537	EARLIER APPLICATION NUMBER: PCT/US97/11825			
Qy	541 RIAIAARALVRNPKILLDEATSDALTESRQVALDKARKGRTTIVIARLSTVNADY	600	EARLIER FILING DATE: 1999-05-27			
Db	538 RIAIAARALVRNPKILLDEATSDALTESRQVALDKARKGRTTIVIARLSTVNADY	597	NUMBER OF SEQ ID NOS: 16			
Qy	601 IAGFDDSVIVEKGNHDELMKEGIYFKVWTAGNEIELENAADEKSEIDTLENSHD	660	SOFTWARE: Patentin Ver. 2.0			
Db	598 IAGFDDSVIIVEKGNHDELMKEGIYFKVWTAGNEIELENAADEKSEIDTLENSHD	657	SEQ ID NO: 2			
Qy	661 SGSSLIRKSTRSRSVGSQGDRKLSTKEALDESIPPSFRIMKLNLTENPYFVGFPC	720	LENGTH: 1280			
Db	658 SGSSLIRKSTRSRSVGSQGDRKLSTKEALDESIPPSFRIMKLNLTENPYFVGFPC	717	TYPE: PRT			
Qy	721 AINGGLQPAFAVIFSKIGIFTRNDDBTKRNSNULSFLLPLVGLTYSFTTFLOGFTF	780	ORGANISM: Homo sapiens			
Db	718 AINGGLQPAFAVIFSKIGIFTRNDDBTKRNSNULSFLLPLVGLTYSFTTFLOGFTF	777	FEATURE:			
Qy	781 GKAGBLITKRLRYMFSSMLRDVSFWDPTKNTGALTTRLANDAQVKGAGSLRAIT	840	OTHER INFORMATION: Human MDR 185-G			
Db	778 GKAGBLITKRLRYMFSSMLRDVSFWDPTKNTGALTTRLANDAQVKGAGSLRAIT	837	SEQ ID: 09-584-586-2			
Qy	841 QNANLGTGIIISLIYGRQLTLLIAITPIIAITAGVEMKMLSGQALKDKELEGAKIA	900	SEQ ID: 1238			
Db	838 QNANLGTGIIISLIYGRQLTLLIAITPIIAITAGVEMKMLSGQALKDKELEGAKIA	897	Best Local Similarity 96.4%; Score 6212.5;			
Qy	901 TEAIENFRTVSLTQDKPERMYDOSCPYNSLRKAHIFGIFTFSPTOMMYFSYACCF	960	Pred. No. 0;			
Db	898 TEAIENFRTVSLTQDKPERMYDOSCPYNSLRKAHIFGIFTFSPTOMMYFSYACCF	957	Matches 1238; Conservative 18; Mismatches 24; Indels 8			
Qy	961 RFGAYLVASHLMSFEDVLLVPSAVVFGAMAVGQVSSPAPDYAKAKYSAAHIMIIEKTP	1020	Gaps 1;			
Db	958 RFGAYLVASHLMSFEDVLLVPSAVVFGAMAVGQVSSPAPDYAKAKYSAAHIMIIEKTP	1017	Query Match 96.4%; Score 6212.5;			
Qy	1021 IDSYSTEGLKPNPLLEGNTVNFNTVPLQPSLIPVLOLSSLTVEYKGTLLALVGSSGCKS	1080	Best Local Similarity 96.5%; Pred. No. 0;			
Db	1018 IDSYSTEGLKPNPLLEGNTVNFNTVPLQPSLIPVLOLSSLTVEYKGTLLALVGSSGCKS	1077	Matches 1238; Conservative 18; Mismatches 24; Indels 8			
Qy	1081 TVVQOLLERFYDPLAKVLLDGKEIKQLNQVWLRAHGLIVSQEPILFDOSISENIAYGDNS	1140	Match 96.4%; Score 6212.5;			
Db			Pred. No. 0;			

Query Match, Best Local Similarity	96.3%	Score 6203.5;	DB 2;	Length 1280;				
Matches 1237; Conservative	96.4%;	Pred. No. 0;	Indels 25;	Gaps 1;				
Qy	1	M DLEGRDNGA EKKNPFLANKSKDKCERKPTVSYEMRYSNWLQKLMTYGTLLAI 60	Db	Db	1018	IDSYSTEMGLNTLEGANTVFTGEVVFNYPTPDIPLVQLQSLEVKKGOTLAVGSGCRS 1077		
Db	1	M DLEGRDNGA EKKNPFLANKSKDKCERKPTVSYEMRYSNWLQKLMTYGTLLAI 60	Qy	Qy	1081	TYVQLERPYDPLAKVYLQDGKEITKQLYTQMLRHLGIQSOPBILFDCS1ENTAYGDNS 1140		
Qy	61	H GAGLPLMLVFGMTDIFANGNLGDLALLFANTISSNITDTPVYMLLEDMDTRAYY 120	Db	Db	1078	TYVQLERPYDPLAKVYLQDGKEITKQLYTQMLRHLGIQSOPBILFDCS1TAENTAYGDNS 1137		
Qy	61	H GAGLPLMLVFGMTDIFANGNL--LMENITRSINDTGFFNLEDMDTRAYY 117	Qy	Qy	1141	RVVSQEPIVRAAKEANIAHAPTESLPNKYSTRGDGTGKOTLGGQKORIATALARLYTOPHIL 1200		
Db	121	YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 180	Db	Db	1138	RVVSQEPIVRAAKEANIAHAPTESLPNKYSTRGDGTGKOTLGGQKORIATALARLYTOPHIL 1197		
Qy	118	YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 177	Qy	Qy	1201	LDEATASALDPESEKTVQBALDKAREGRCTCIVIAHRLSTIONADLJUVFONGRVKEHGHT 1260		
Db	178	DVSCKINEGDKGMFFQSMATFTGFTGFTREWKLTVILATISPVGLSAAWAKLIS 240	Db	Db	1198	LDEATASALDPESEKTVQBALDKAREGRCTCIVIAHRLSTIONADLJUVFONGRVKEHGHT 1257		
Qy	241	SFTDKELLA YAKGAVAEEVLAARTVIAFGQQKKELEMYKONBEAKRIGKATAIANI 300	Qy	Qy	1261	QOLLAKGQIYFSMVSYQAGKQ 1283		
Db	238	SFTDKELLA YAKGAVAEEVLAARTVIAFGQQKKELEMYKONBEAKRIGKATAIANI 297	Db	Db	1258	QOLLAKGQIYFSMVSYQAGKQ 1280		
RESULT 11								
		US-09-817-762-3						
		Sequence 3; Application US/99817762						
		Patent No. 6838774						
		GENERAL INFORMATION						
		APPLICANT: Spalding, Edgar P.						
		APPLICANT: No. 6858774, Boell						
		TITLE OF INVENTION: ABC Transporter Gene From						
		Plants						
		FILE REFERENCE: 11238-00061						
		CURRENT APPLICATION NUMBER: US/09/817,762						
		PRIOR APPLICATION NUMBER: PCT/US99/22363						
		PRIOR FILING DATE: 1999-09-24						
		PRIOR APPLICATION NUMBER: US 60/101,814						
		PRIOR FILING DATE: 1998-09-25						
		NUMBER OF SEQ ID NOS: 14						
		SOFTWARE: FastSEQ for Windows Version 4.0						
		SEQ ID NO 3						
		LENGTH: 1280						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		PUBLICACION INFORMATION						
		DATABASE ACCESS NUMBER: Genbank P08183						
		DATABASE ENTRY DATE: 1997-11-01						
		US-09-817-762-3						
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		Best Local Similarity 96.4%; Pred. No. 0;						
		Indels 3; Gaps 1;						
		Matches 1237; Conservative						
		18; Mismatches						
		25; InDelNtRSIDN1DGTFMNLEEDMTRYAY 117						
		1 MDLEGDRNGCAEKKNFPCUNNKSBDKCKERKPTVSFSMFRYSNWLQKLMTYGTLLAI 60						
		1 MDLEGDRNGCAEKKNFPCUNNKSBDKCKERKPTVSFSMFRYSNWLQKLMTYGTLLAI 60						
		61 HGAGIPLMLVFGDMTDPPAGNLGDGLAL1FNTNTSSN1DTDTVPMNLLEEDMTRYAY 120						
		61 HGAGIPLMLVFGDMTDPPAGNLGDGLAL1FNTNTSSN1DTDTVPMNLLEEDMTRYAY 120						
		61 HGAGIPLMLVFGDMTDPPAGNLGDGLAL1FNTNTSSN1DTDTVPMNLLEEDMTRYAY 117						
		121 YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 180						
		121 YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 180						
		118 YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 177						
		118 YSGIGAGTVYAAVYIQSPVCLAAQRQHICRKIRKOFHALMROBGFWDVHGBLNTPLTD 177						
		181 DVSKINNEGIGDKIGMFQSMATFTGFTGFTGWKLTVLVIAISPVGLSAAWAKLIS 240						
		178 DVSKINEVIGDKIGMFQSMATFTGFTGFTGWKLTVLVIAISPVGLSAAWAKLIS 237						
		241 SFTDKELLA YAKGAVAEEVLAARTVIAFGQQKKELEYNLEARIGIKKATANI 300						
		238 SFTDKELLA YAKGAVAEEVLAARTVIAFGQQKKELEYNLEARIGIKKATANI 297						
		301 STGAFFLIIYASYALAFWYTTLVLSKEYSIGVLTVPFSVLLIGAFSYQASPSIEAFAN 360						
		301 STGAFFLIIYASYALAFWYTTLVLSKEYSIGVLTVPFSVLLIGAFSYQASPSIEAFAN 360						

298 SIGAAFLIIVASYALAFWYGTTLVLSGEYSIGQVLTVFSVGOASPSTEAFAN 357
 Db 361 ARGAAPFICLIDNKESIDTSKSGHKPKDNFKGNEFRATHFYSRSRKETKILKGLNLKV 420
 Qy 358 ARGAAPFICLIDNKESIDTSKSGHKPKDNFKGNEFRATHFYSRSRKETKILKGLNLKV 417
 Db 421 QSGQTVALGENSGCGKSTTQLMORLYDPTGCMVSUDGQDIRTINRFLBELLGIVVSQP 480
 Qy 418 QSGQTVALGENSGCGKSTTQLMORLYDPTGCMVSUDGQDIRTINRFLBELLGIVVSQP 477
 Db 481 VLFATTIAENRYGRBDVTHDEIKAVKANEAYDFIMCLPKPDFLVGERGAOLSGGQKQ 540
 Qy 478 VLFATTIAENRYGRBDVTHDEIKAVKANEAYDFIMCLPKPDFLVGERGAOLSGGQKQ 537
 Db 541 RIAIAALAVRNPKILLDEATSALDTESEAQQVALDKARKRITIVIAIRLSTVNADY 600
 Db 538 RIAIAALAVRNPKILLDEATSALDTESEAQQVALDKARKRITIVIAIRLSTVNADY 597
 Qy 601 IAGFDGTVYERGNHDBLMKRGKGITYPKLVTMOTAGNIBLENAADRSKSEIDTLEMSSID 660
 Db 598 IAGFDGTVYERGNHDBLMKRGKGITYPKLVTMOTAGNIBLENAADRSKSEIDTLEMSSID 657
 Qy 661 SGSSLIRKRSTRSRVSGQGDRLKSTKEALDESIPPVSPTRIMCLNLTEMPYFVGVR 720
 Db 658 SRSSLRKRSTRSRVSGQADRKLSKTEALDESIPPVSPTRIMCLNLTEMPYFVGVR 717
 Qy 721 AINGGLQPAATIFSKIGITFRNDAAETRKNSNLPSLFLYGVISFTFLFQGTF 780
 Db 718 AINGGLQPAATIFSKIGITFRNDPETRKNSNLPSLFLGIIISFTFLFQGTF 777
 Qy 781 GKAGETLTKRLYMVFRSMLRQDSWFDPKNTGALTTRIANDAQVKAIGSLAIT 840
 Db 778 GRAEGLTKRLYMVFRSMLRQDSWFDPKNTGALTTRIANDAQVKAIGSLAIT 837
 Qy 841 QNANIGTGIIISLIVGMQVLTLLIAIIPITIAIAGVEMOMLSGOALKRKELEGAKIA 900
 Db 838 QNANIGTGIIISLIVGMQVLTLLIAIIPITIAIAGVEMOMLSGOALKRKELEGAKIA 897
 Db 901 TEAIENFRTVSLTQOKPERMTDQLPQTPRSRKAHFGITSPQTMAYESYAGCF 960
 Db 898 TEAIENFRTVSLTQOKPERMTDQLPQTPRSRKAHFGITSPQTMAYESYAGCF 957
 Qy 961 RFGATLVASHSISFEDVLYPSAVFEGAMAQVQVSSPAFYAKVSAHIMIETKTPL 1020
 Db 958 RFGATLVASHSISFEDVLYPSAVFEGAMAQVQVSSPAFYAKVSAHIMIETKTPL 1017
 Qy 1021 IDSYSTEGLKENTLEGNTFVKEVVPYTPTRDIPVQGLSLSEVKGGQTLALVGSSGCKS 1080
 Db 1018 IDSYSTEGLKENTLEGNTFSEVVFNYTPTRDIPVQGLSLSEVKGGQTLALVGSSGCKS 1077
 Qy 1081 TUVOLLERFDPPLAGTVLJLDCKEIKLNVQWRAHGIYGSOBPLFDCSISENTAGDNS 1140
 Db 1078 TVVOLLERFDPPLAGTVLJLDCKEIKLNVQWRAHGIYGSOBPLFDCSISENTAGDNS 1137
 Qy 1141 RVVSOBEITRAKEANTHAFALESPLNKKSYTVPGDKTQLSGQKORIALARVOPHL 1200
 Db 1138 RVVSOBEITRAKEANTHAFALESPLNKKSYTVPGDKTQLSGQKORIALARVOPHL 1197
 Qy 1201 LLDEATSDTESEVVQEAIDKAREGRCTIVIAIRLSTIONADLIVVONGRVEHGH 1260
 Db 1198 LLDEATSDTESEVVQEAIDKAREGRCTIVIAIRLSTIONADLIVVONGRVEHGH 1257
 Qy 1261 QLLAOKGITYPSMSVYOAQAKRQ 1283
 Db 1258 QLLAOKGITYPSMSVYOAQAKRQ 1280

; APPLICANT: Bunting, Kevin ; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 ; TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 ; FILE REFERENCE: 1340-1-021CIP
 ; CURRENT APPLICATION NUMBER: US/09/584,586
 ; EARLIER APPLICATION NUMBER: US 60/086,988
 ; EARLIER FILING DATE: 1988-05-28
 ; EARLIER APPLICATION NUMBER: PCT/US99/11825
 ; EARLIER FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 4
 ; LENGTH: 1280
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Human MDR 185-V
 ; US-09-584-586-4

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
 Best Local Similarity 96.4%; Pred. No. 0; Mismatches 25; Indels 3; Caps 1;
 Matches 1237; Conservative 18; Miatches 1;

Qy 1 MDLIEDGDRNGAECBKNNFKLANKSGKDKGGERKPTVFSMFRYSNWLDKLYMVVGTLAAII 60
 Db 1 MDLIEDGDRNGAECBKNNFKLANKSGKDKGGERKPTVFSMFRYSNWLDKLYMVVGTLAAII 60
 Qy 61 HGAGLPLMLVFGDMTDFANACNLGDLGALLFNNTNSNITDTDVPMANBEDMTYAY 120
 Db 61 HGAGLPLMLVFGDMTDFANACNLGDLGALLFNNTNSNITDTDVPMANBEDMTYAY 117
 Db 121 YSGIGAGLULVARVQSFPCWLAAGRQTHKIRKQFFAHMROEIGWPDVHDGELNTRLTD 180
 Db 118 YSGIGAGLULVARITQVSPWCLLAGRQTHKIRKQFFAHMROEIGWPDVHDGELNTRLTD 177
 Qy 181 DVSKINEGIGDKIGMFFQSMATEPTGFTVGFGRGMKLTLYLVAISPVLGSAVWKILS 240
 Db 178 DVSKINEVIGDKIGMFFQSMATEPTGFTVGFGRGMKLTLYLVAISPVLGSAVWKILS 237
 Qy 241 SFIDRELLAYAKAGAABEVLANIRTYAEGQKKELEERYNKNLBAKRIGKIKKATANI 300
 Db 238 SFIDRELLAYAKAGAABEVLANIRTYAEGQKKELEERYNKNLBAKRIGKIKKATANI 297
 Qy 301 SIGAFLIYIAYALAFYGTTLVLSKEYSIGVOLTVFSSVJIGASVQGOSPIRAFAN 360
 Db 298 SIGAFLIYIAYALAFYGTTLVLSKEYSIGVOLTVFSSVJIGASVQGOSPIRAFAN 357
 Qy 361 ARGAAFEIPKIDONKPSIDSYSKGHKPDKNIGNLNFRVNHFSYSPRSKEVVLKGNLKV 420
 Db 358 ARGAAFEIPKIDONKPSIDSYSKGHKPDKNIGNLNFRVNHFSYSPRSKEVVLKGNLKV 417
 Qy 421 QSGTVALVGNSCGKSTVQMLORLYDPTGEMSVYDQGDIRTINYRFLREITGVYQEP 480
 Db 418 QSGTVALVGNSCGKSTVQMLORLYDPTGEMSVYDQGDIRTINYRFLREITGVYQEP 477
 Qy 481 VLPATTAENIRGREDYTMDEIKAVENTANAYDFINKLPKPDPLVGERGQLSGGOKO 540
 Db 478 VLPATTAENIRGREDYTMDEIKAVENTANAYDFINKLPKPDPLVGERGQLSGGOKO 537
 Qy 541 RIALARALVNPKILLDEATSDATESVQVALIDKARKRTTIVIAHRLSTVNRADV 600
 Db 538 RIALARALVNPKILLDEATSDATESVQVALIDKARKRTTIVIAHRLSTVNRADV 597
 Qy 601 IAGFDGTVKEKENHDELMKRGKSYFQGDPLKSTKEALDSEIPPSYFRIMKLNTWMPYFVGFC 720
 Db 598 IAGFDGTVKEKENHDELMKRGKSYFQGDPLKSTKEALDSEIPPSYFRIMKLNTWMPYFVGFC 717

RESULT 12
 DE-09-584-586-4
 Segment 4, Application US/09584586
 Serial No. 6933150
 Serial Information:
 Brian Sorrentino, Brian

661 SGSLIIRKSTRRSYRSQGDPLKSTKEALDSEIPPSYFRIMKLNTWMPYFVGFC
 658 SRSSLRKSTRRSYRSQGDPLKSTKEALDSEIPPSYFRIMKLNTWMPYFVGFC